



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 162981

TO: **Phuong Bui**
Art Unit: **1638**
Location: **REM-2A15&2C18**
Serial Number: **10/660226**

Wednesday, August 31, 2005

From: **Beverly Shears**
Location: **Biotech-Chem Library**
REM 1A54
Phone: **571-272-2528**
beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
A	1	574	47.8	1061	8	BT009529 Triticum
	2	501.2	41.8	1918	8	AK109730 Triticum sat
	3	423.4	35.3	1356	8	AK066687 Oryza sat
	4	364.4	30.4	1323	8	BT009514 Triticum
	5	242.4	20.2	1293	8	LESHKINP
	6	242.4	20.2	1303	8	BT012939 Lycopersai
	7	237.8	19.8	1300	8	AK111889 Arabidops
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	11	185.8	15.5	1016	8	AY596190 Cucumis s
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	18	85.4	7.1	137740	1	D90900 Synecocyst
C	19	84.8	7.1	137843	8	BT012407 Arabidops
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Qy      467  TGTGGGGAAGATTATCTCTGAAAGTC TGTGGTTATTCTGTTCTTTGATAGTGACAAAGTTAGT 526
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Qy      767  TGGCTCTGCTCTCTTCTGGAACCAACCATCTGGTGTATCCGTAGCGAATGGCCCTTTTCTAA 826
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Qy      887  TCTGGAAGAGATTGCATGTAAACAAGSTCATGATGATGCTCTTAAGCTGACACCTACTGA 946
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RESULT 2
AKI09730
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:002-146-B12, full
insert sequence.
AKI09730
VERSION
AKI09730.1 GI:32994939
KEYWORDS
FLI CDNA; oligo capping.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1
REFERENCE
1
AUTHORS
The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team:
Kikuchi S., Sato K., Nagata T., Kawagashira N., Doi K.,
Kishimoto N., Yazaki J., Ishikawa M., Yamada H., Ooka H., Hotta I.,
Kojima K., Namiki T., Ohneda E., Yahagi W., Suzuki K., Li C.,
Ohtsuka K., Shishiki T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Ootomo Y., Murakami K.,
Iida Y., Sugano S., Fujimura T., Suzuki Y., Tsunoda Y.,

```

TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 Science 301 (5631), 376-379 (2003)
 22752273
 12869764
 2 (bases 1 to 1918)
 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ihibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Kato,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Nariakawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Ootomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toyota,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.

TITLE JOURNAL

Direct Submission
 Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
 This clone is one of the 28K full-length cDNA clones from japonica rice.

COMMENT

URL : http://cdna01.dna.affrc.go.jp/cDNA/
 NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
 PAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Nariakawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Kato,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Saeki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toyota,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
 Location/Qualifiers
 1..1918
 /organism="Oryza sativa (japonica cultivar-group)"

FEATURES source


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/mol_type="mRNA"  
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ORIGIN	Query Match	41.8%; Score 501.2; DB 8; Length 1918;
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	Matches 600; Conservative 0; Mismatches 143; Indels 3; Gaps 1;	
QY	338 AGTGCATGAAACTCGCACAACTCCGTGACGAAGCTCTCCCTGTTGCAAGGAAATTCACA	397
Db	982 AGCCACGACAGCTGCATAACTCAGTTGATGAAGCCCTCCCTGTTAAAGAGGAAATTCACA	1041
QY	398 AGAAGTCTCTTCTACTTGAACGGGAGGTGTATTTACCTAGTAGGAGTAATGATGGTTCCTCG	457
Db	1042 AGAAGTCTTATCTACTTGAACGGGAGGTGTATTTATTTAGTTGGAATGATGGCTCAGG	1101
QY	458 AAAAAGTACTGTGGGGAAGATATGTCGTAAGTCTTGGGTATTCGTTCTTTGATAGTGA	517
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Db	1702 CTTGTAGAAATTTTGGCCCTCTCTTTTTT	1727

RESULT 3

AK066687

LOCUS

DEFINITION

ORyza sativa (japonica cultivar-group) cDNA clone:J013074B04, full insert sequence.

ACCESSION

AK066687

VERSION

AK066687.1 GI:32976705

KEYWORDS

FLI CDNA; CAP trapper.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

REFERENCE
AUTHORS

1 The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, K., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, K., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)

JOURNAL
MEDLINE
PUBMED

22752273
12869764

REFERENCE
AUTHORS

2 (bases 1 to 1356)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Itoh, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyu, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuka, K., Oka, M., Ooka, H., Ootomo, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Tova, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

TITLE
JOURNAL

Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan [E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007]
This clone is one of the 28K full-length cDNA clones from japonica rice.

COMMENT

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T. and Yamamoto, M.
FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,

Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
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ORIGIN

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 Matches 558; Conservative 0; Mismatches 96; Indels 47; Gaps 3;
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 DB 83 GGAGGCGGCGTGGGCGTGGCGTGCAGTGGGGCGGGGTTCCGGCGCTCCGACCG 142
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 QY 311 CGGACTCCGTGGCAAGAAATCGTCGGAGGTGATGAAACTCGCAAACTCCGTTGACGA 370
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 QY 371 AGCTCTCTGTTGAAGAGAAATCAGAAGATTTCTGTTCTACTTGAACGGGAGGTGAT 430
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 QY 431 TTACCTAGTAGGAATCATGGTTCTGGAAGAAAGTACTGTGGGAAGATTTGCTGAAGT 490
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 QY 791 ACCATCTGGTGATCCGTGACCAATGGCTTTTCTAAGCTCA 831
 DB 714 ACCATCTGGTGATCCATACCAATGGTGACTACTTGGCCCA 754

RESULT 4
 BT009514

LOCUS BT009514 1323 bp mRNA linear PLN 20-JUN-2003
 DEFINITION Triticum aestivum clone wri.pk0099.b12:fis, full insert mRNA
 sequence.
 ACCESSION BT009514
 VERSION BT009514.1 GI:32129065
 KEYWORDS FLI CDNA.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 1323)
 Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
 Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
 Direct Submission
 Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
 Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
 USA
 Location/Qualifiers
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 Query Match 30.4%; Score 364.4; DB 8; Length 1323;
 Best Local Similarity 71.9%; Pred. No. 2.4e-70;
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 QY 393 TCAGAAGAAGTTCTGTTCTACTTTGAACGGGAGGTGATTTACTAGTAGGAATGATGGT 452
 DB 230 CGAGAGGACGTGCTCCCTTACCTGAATGACCGCTGTGTTATCTAGTTGGAATGATGGT 289
 QY 453 TCTGAAAAAGTACGTGGGGAAGATTATGCTGAAGCTTGGGTATTCGTTCTTTGAT 512
 DB 290 TCCGCAAAACTACAGTTGGGAAGATAATAGCTGAAGTACTAGGCTATTTCATTCTTTGAC 349
 QY 513 AGTCACAAAGTTAGTGAGCAAGCTGTTGGAATGCCATCAGTTGCCCAATATTCAAGGTC 572
 DB 350 AGTGATAGCTGTTGAGCAGCTCTGTGGCATACCGTCGCTGGCTGAGATTTTCAGGTC 409
 QY 573 CATAGTGAAGCCTTCTTTCCGGATTAATGAGAGTAGTGTCTTGAGAGATTTGCTCCATG 632
 DB 410 CACAGTGAAGCAATCTTTCAGAGATAACGAGAGTGAGTACTAAGGGATTTGTCGTCATG 469
 QY 633 CGACGATTAGTTGTTGCCACCGGAGGTGGTCTGTTATCCGACCAATTAACCTGGAGATAT 692
 DB 470 CACCATTAAATTTGTCACACAGGAGGTGGTGGGGTATACGACCAATCAATTTGGAGTTAT 529
 QY 693 ATGAAGAGGGGCTATCTGTTTGGTTAGATGTGCCCTTTGGATGCTCTTCTGCTAGGGGTAT 752
 DB 530 ATGAAGAAAGGACTCACTATTGTTGGTTAGATGTTCCATTGGACGCCCTTGCAGAGAGAT 589
 QY 753 GCTAAAGTGGGAATGCGCTCTCGTCTCTTTCTGGACCAACCATCTGGGTGATCGGTACGCA 812
 DB 590 GCTGGGTTGGTACTCTGGCTACGACGCCCTCTCGCATCAGGAATCTGGTATCTTATGCA 649
 QY 813 ATGGGCTTTTCTTAAGCTCAGCATGTTGCACACAAAGGGGTGATGCTTATCAATGCA 872
 DB 650 AAGGCTATGCGCAAACTTACACACTTTTGAACAAAGAAATGGATTCATATGCTAATGCT 709
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 DB 710 GATGCCGAGTTTCCCTTGAAATATTGCAATTCANACAAGGACATAATGATGTAATGTA 769
 QY 933 CTGACACCTTATGATATTGCAATGAGTCACTTCATAAGATCGAGAGCTTCGTCATCGAG 992
 DB 770 CTTACACCAAGTGCCATCGCTATTGAGGCAATGCTAAAGATGGAGAGCTTTCTTACTGAG 829

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QY 993 CA 994
Db 830 AA 831

LESHKINP 1293 bp mRNA linear PLN 16-JUN-1992
LOCUS L.esculentum mRNA for shikimate kinase precursor.
DEFINITION X63560
ACCESSION X63560
VERSION 1
KEYWORDS shikimate kinase.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 1293)
Schmid,J., Schaller,A., Leibinger,U., Boll,W. and Amrhein,N.
The in-vitro synthesized tomato shikimate kinase precursor is
enzymatically active and is imported and processed to the mature
enzyme by chloroplasts
Plant J. 2 (3), 375-383 (1992)
JOURNAL
MEDLINE 93272054
PUBMED 1338949
REFERENCE 2 (bases 1 to 1293)
Schaller,A.
Direct Submission
Submitted (27-DEC-1991) A. Schaller, Federal Institute of
Technology, Institute of Plant Sciences, Sonnegstrasse 5, 8092
Zuerich, SWITZERLAND
FEATURES
Source
1. .1293
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/strain="UCD2b"
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123. .1025
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/db_xref="GI:19349"
/db_xref="GOA:Q00497"
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mat_peptide 321. .1022
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/EC_number="2.7.1.71"

ORIGIN
Query Match 20.2%; Score 242.4; DB 8; Length 1293;
Best Local Similarity 62.7%; Pred. No. 3.4e-43;
Matches 394; Conservative 0; Mismatches 231; Indels 3; Gaps 1;

QY 360 TCCGTTGACGAAGCTCTCCTGTTGAAGAGAAAATCAGAGAAGTTCTGTCTACTTGAAC 419
Db 372 TCAATTGATGAATCGACACATTAAGAATAAGCAGAGAAGTTGAAGAATATCTAGAT 431
QY 420 GCGAGGTGTATTACTAGTAGAATGATGGGTTCTGGAAAAAGTACTGTGGGAAGATT 479
Db 432 GCACGATGTGTATACCTTGTGGAATCATGGGCTGCGGAAAAACAACCTGTGGCCGGATT 491
QY 480 ATGCTCGAAGCTTTGGGTTATTCGTTCTTTGTAGTGACAAGTACTGGGCAAGCTGTT 539
Db 492 TTGGCAAAACACTGGGATATTCCTTTTGTACTGTGACAGGCTGATAGACGGCTGTT 551

RESULT 6
BT012939 1303 bp mRNA linear PLN 11-MAY-2004
LOCUS Lycopersicon esculentum clone 114107R, mRNA sequence.
DEFINITION BT012939
ACCESSION BT012939
VERSION 1
KEYWORDS FLJ_CDNA.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 1303)
Kirkness,E.F., Wang,W. and Vazeille,A.
Direct Submission
Submitted (11-MAY-2004) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20850, USA
FEATURES
Source
1. .1303
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
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/cloned="114107R"
/tissue_type="mature green fruit"
/note="TWGE47"

ORIGIN
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Best Local Similarity 62.7%; Pred. No. 3.4e-43;
Matches 394; Conservative 0; Mismatches 231; Indels 3; Gaps 1;

QY 360 TCCGTTGACGAAGCTCTCCTGTTGAAGAGAAAATCAGAGAAGTTCTGTCTACTTGAAC 419
Db 344 TCAATTGATGAATCGACACATTAAGAATAAGCAGAGAAGTTGAAGAATATCTAGAT 403
QY 420 GCGAGGTGTATTACTAGTAGAATGATGGGTTCTGGAAAAAGTACTGTGGGAAGATT 479
Db 404 GCACGATGTGTATACCTTGTGGAATGATGGGCTGCGGAAAAACAACCTGTGGCCGGATT 463
QY 480 ATGCTCGAAGCTTTGGGTTATTCGTTCTTTGTAGTGACAAGTACTGGGCAAGCTGTT 539

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ACCESSION AK117791.1 GI:26450650
 VERSION FLI CDNA; CAP trapper.
 KEYWORDS Arabidopsis thaliana (thale cress)
 SOURCE Arabidopsis thaliana
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinzaki, K.
 TITLE Arabidopsis thaliana full-length cDNA
 JOURNAL Published Only in Database (2002)
 REFERENCE 2 (bases 1 to 1294)
 AUTHORS Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinzaki, K.
 TITLE Direct Submission
 JOURNAL Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: msekigsc.riken.go.jp, URL: http://pfweb.gsc.riken.go.jp, Tel: 81-45-503-9625, Fax: 81-45-503-9586)
 COMMENT An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and SalI. This clone is in a modified pBluescript vector.
 Please visit our web site (http://pfweb.gsc.riken.go.jp/) for further details.
 FEATURES
 Location/Qualifiers
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 /ecotype="Columbia"
 /note="common name: thale cress"
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 /gene="At4g39540/F23K16_170"
 CDS 228..1130
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 Best Local Similarity 59.0%; Pred. No. 3.3e-32;
 Matches 369; Conservative 0; Mismatches 250; Indels 6; Gaps 2;
 QY 363 GTTGCAAGAGCTCTCCTGTTGAAGAGAAAATCAGAGAAGTTCTGTTCTACTTTGAACGGG 422
 Db 462 GATGAAGACAACAGATTTTGAGAAAAAAGCTGAAGAGTTAAACCGTATTAAATGGA 521
 QY 423 AGGTGTTATTACTAGTAGAATGATGGTTCGGAAGAAAGTACTCTGGGGAAGATTATG 482
 Db 522 CGATCATGTATCTTGTGTTATGATCGGTTCCGGGAAAACGACTGTAGGGAAGATTATG 581
 QY 483 TCTGAAGTCTTGGTATTCTGTTCTTTGATGACAACTTAGTGAGCAAGCTGTTGGA 542
 Db 582 GCAAGATCGCTTGGTATTACATTTCTTTGATTGTGACACTTTTGTATCGAGCGGCTATGAAG 641

QY 543 ATGCCATCAGTTGCCCAAAATATTCAAGGTCATAGTAGAAGCCCTTCTTTGGGATAATGAG 602
 Db 642 GGAACTTCTGTAGCTCAGATATTGAGCATTTTCGGTGAGAGTGTCTTTCAAGAGAAAAGAG 701
 QY 603 AGTAGTGTCTTGAGAGATTGTCTCCATG---CGACGATTAGTTGTTGCCACCGGAGGT 659
 Db 702 ACTGAAGCGTTAAGAAACTCTCTTTGATGTATACCACCAAGTTGTTGTTTCAACCGGGGA 761
 QY 660 GGTGCTGTTTATCGACCAATTAACCTGAGATATATGAAGAGGGGCGCTATCTGTTTGGTTA 719
 Db 762 GGGGCAATTATGAAGCCCATCAATGGAAGTACATCATTAAGGTAATTAGTATTGGCTT 821
 QY 720 GATGTCCTTGGATGCTCTTGTAGCGGTATTGTCTAAAGTGGGAAGTCTCTCTGTCCT 779
 Db 822 GATGTACTCTAGAAGCCTTAGCGCATAGATAGTGTCTGTAGGAAGTGTGTTCAAGACCA 881
 QY 780 CTTCTG--GACCAACCATCTGGTATCGTAGGCAATGGCCTTTTCTAAGCTCAGCATG 836
 Db 882 TTGCTCATGATGATGAGTCAGGGGACACATACACAGCGGCTTTAAACCGTCTTTCAACG 941
 QY 837 CTTGCACAGCAAAAGGGGTGATGCTTATGCAAAATGCAGATGTAAAGGTTTCTCTGGAAGAG 896
 Db 942 ATTGGGATGCAGTGTGTGAGCATACATAAAGCCAGCGCAGAGATTTCTTTGGAGAT 1001
 QY 897 ATTGCATGTAAACAAAGGTCATGATGATGCTCTTAAGCTGACACCTACTGATATTGCAAT 956
 Db 1002 ATTACTTTGAAGCTCGTTTATAGAAGTGTCTCAGATCTTTACACCACTGAAATCGCAAT 1061
 QY 957 GAGTCACTTCATAAGATCGAGAGCT 981
 Db 1062 GAGGCTTTTGAGCAAGTTCAGAGCT 1086
 RESULT 11
 AY596190
 LOCUS Cucumis sativus shikimate kinase mRNA linear PLN 04-MAY-2004
 DEFINITION Cucumis sativus shikimate kinase mRNA, partial cds.
 ACCESSION AY596190
 VERSION AY596190.1 GI:46849855
 KEYWORDS Cucumis sativus (cucumber)
 SOURCE Cucumis sativus
 ORGANISM Cucumis sativus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
 REFERENCE 1 (bases 1 to 1016)
 AUTHORS Kim, M.S., Yang, K.Y., Kim, Y.C. and Cho, B.H.
 TITLE A shikimate kinase and an acidic peroxidase gene expression were primed by a rhizobacterial colonization upon challenge-inoculation with *Corynebacterium cassicola* in cucumber leaves
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1016)
 AUTHORS Kim, M.S., Yang, K.Y., Kim, Y.C. and Cho, B.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-APR-2004) Applied Plant Science Division, Chonnam National University, Yongsong Dong 300, Bukgu, Gwangju 500-757, Korea
 FEATURES
 Location/Qualifiers
 1..1016
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 /db_xref="GI:46849856"
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 CDS
 ORIGIN

Query Match	15.5%;	Score 185.8;	DB 8;	Length 1016;	
Best Local Similarity	61.8%;	Pred. No. 1.3e-30;			
Matches 295;	Conservative	0;	Mismatches 182;	Indels	0; Gaps 0;
QY	549	TCAGTTGGCCCAATATTCGAAGTCCATAGTGAAGCCTTCTTTCCGGGATAATCAGAGTAGT	608		
Db	7	TCTGTAGCCGAAAGTTTCAAGGTCTATGGGGAGCACTTCTTTAGAGAAAGGAGCGGAA	66		
QY	609	GTCCTGAGAGATTGTCCTCCATCGCAGCAATAGTTGTTGGCCACCGGAGTGGTCTGTT	668		
Db	67	GCAATTGAGAAGTTATCTTTGATGCCCACTTTGTTATTTCACAGCGCGAGGTGCTGTA	126		
QY	669	ATCCGACCATAAATTCGGAGATATATGAAGAGGGGCTATCTGTTTGGTTAGATGTCGCC	728		
Db	127	ACGAGATCGATTAACCTGGAAATATATGCAATGAAGCATCAGTGTGTTGGTTGATGTCCT	186		
QY	729	TTGGATGCTCTTCTAGGCGTATTGCTAAAGTGGGAACCTGCTGCTGCTCTTCTTGGAC	788		
Db	187	TTGGAAGCCTTGTTTGAAGAGAAATTCAGCTGTAGGAACCAATTCGTCGCCCTTTTGCAT	246		
QY	789	CAACCATCTGGTATCCGTACGAATGGCCTTTTCTAAGCTCAGCATGCTTSCACAGCAA	848		
Db	247	CATGATTCAAAATGATCACTCAAGACCCCTCGTCGTTTATCTACTCTCTGGAAGAG	306		
QY	849	AGGGGTGATGCTTATGCAAAATGCAGATGAAGGTTTCTCTGGAAGAGATTGCATGAAA	908		
Db	307	AGGGCGAAGCATATGCCAACGCTGAAGTCAAAAGTTTCTGCGAATAAATTCAGCCAAA	366		
QY	909	CAAGGTCATGATGATGCTCTTAAGCTGCACACCTTACTGATATATGCAATTGAGTCACATTCAT	968		
Db	367	CTGGGTACTAAAGACGTATCGAATGTCACGCCTATGCGCATAGCAATCGAGGCACTCGAA	426		
QY	969	AGATCGAGGCTTCGTCATCGAGCACATGCTGATAGTTCAGTCAGCAGCGGCAA	1025		
Db	427	GAATCGAGACCTTTTGAAGAGAGAAGATGGTTATTGTGCATTTTGTATGATGACCACAA	483		
RESULT 12					
AK067948					
LOCUS	AK067948				
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone:J013123F09, full insert sequence.	2127 bp	mRNA	linear	PLN 24-JUL-2003
ACCESSION	AK067948				
VERSION	1	GI:32977966			
KEYWORDS	FLI_CDNA; CAP trapper.				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
REFERENCE	1				
AUTHORS	The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team; Kikuchi, S., Satoh, K., Negata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, T., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ohtsuka, T., Iida, J., Imamura, K., Imotani, K., Kawai, J., Itoh, M., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nariikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.				
TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice				
JOURNAL	Science 301 (5631), 376-379 (2003)				
MEDLINE	22752273				
PUBMED	12869764				
REFERENCE	2	(bases 1 to 2127)			
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Atakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, I., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Ikeda, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kondo, S., Konno, H., Kouda, M., Kusumegi, T., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuka, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ohtsuka, T., Saitoh, H., Saitoh, K., Sato, K., Shibata, K., Sakai, C., Sakai, K., Suganawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Shinyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yanada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan [E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007]				
COMMENT	This clone is one of the 28K full-length cDNA clones from japonica rice. URL : http://cdna01.dna.affrc.go.jp/cDNA/ NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T. and Yamamoto, M. FAIS Genome Sequencing & Analysis Group: Ohtsuka, T., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y. Location/Qualifiers 1. :2127 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nipponbare" /db_xref="taxon:39947" /clone="J013123F09"				
ORIGIN					
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Best Local Similarity	69.8%;	Pred. No. 8.3e-26;			
Matches 222;	Conservative	0;	Mismatches 96;	Indels	0; Gaps 0;
QY	677	AATTAACTGGAGATATATGAGAGGGGCTATCTGTTGGTTAGATGTCCTTGGATGC	736		
Db	1584	AATTGTCAGGAGTTACATGAAGAAGGGTCAACAATCTGTTAGATGTTCCATTTGATGC	1643		


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QY 737 TCTGTAGCGGTATTCGTAAGTGGGAAGTGCCTCTCGTCTCTTCTGGAACCAACATC 796
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Db 1824 TAGTAATGTGACGACACTTACACCAAGTGCCATTGCTATTGAGGCAATGCTAAAGATGCA 1883
QY 977 GAGCTTCGTCATCGACA 994
Db 1884 GAGCTTCTTACTGAGAA 1901

RESULT 13
AX315616
LOCUS AX315616 309 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 8601 from Patent WO0190366.
ACCESSION AX315616
VERSION AX315616.1 GI:17899043
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Leach,M.D. and Shinkets,R.A.
TITLE Human polynucleotides and polypeptides encoded thereby
JOURNAL Patent: WO 0190366-A 8601 23-NOV-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
1. .309
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Best Local Similarity 69.3%; Pred. No. 2.6e-24;
Matches 214; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

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Db 61 GCAAGAAGAATTCGCTGCTGTAGGAACCGGCTCTCGACCACTCTTGGCATCAGGAATCCGGT 120
QY 801 GATCCGTAGCGAATGCGCTTTTCTAAGCTCAGCATGCTTGCACAGCAAAAGGGGTGATGCT 860
Db 121 GATCCTTATGCAAAAGGCTTATGCAAACTTACGTCACTTTTTCGAGCAAGAAGATGCACTG 180
QY 861 TATGCAATGCGAGATGAAGGGTTTCTCTGGAAGAGATGTCATGTAAACAAGGTATGAT 920
Db 181 TATGCTAATGCTGATGCCAGAGTTTCACTTGAACATATTGCAATTAACCAAGGCCATAT 240
QY 921 GATGCTCTAAGCTGACACCTACTGATATTGCAATTTGATGTCACCTTCAATGATCGAGAC 980
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QY 981 TTGCTCATC 989
Db 301 TTTCCTACC 309

RESULT 14
AP004089/c
LOCUS AP004089 111777 bp DNA linear HTG 21-MAR-2002
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 2 clone
ACCESSION AP004089.1 GI:15281368
VERSION HTG; HTGS_PHASE2.
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE
1 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza;
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
clone:OJ1308_A10
Published Only in Database (2001)
2 (bases 1 to 111777)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (22-AUG-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2; Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakia@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Location/Qualifiers
1. .111777
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="2"
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Matches 133; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 678 ATTAAGTGGAGATATGAGAGGGCCCTATCTGTTAGATGTGCCCTTGATGCT 737
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QY 738 CTTGCTAGCGGTATTGCTTAAAGTGGGAAGTGCCTCTCGTCTCTTCTTGACCAACCATCT 797
Db 64273 CTTGCTAGCGGTATTGCTTAAAGTGGGACTGCCTCCGCTCTCTCTTAGATCAACCATCT 64214
QY 798 GGTGATCCGTACGCAATGCGCTTTTCTAAGCTCA 831
Db 64213 GGTGATCCATACACAATGCTGACTACTTGGGCCA 64180

RESULT 15
AP004774
LOCUS AP004774 154796 bp DNA linear PLN 15-APR-2004
DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,
PAC clone:P0431B06.
ACCESSION AP004774
VERSION AP004774.3 GI:46390195
KEYWORDS
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SOURCE	Oryza sativa (japonica cultivar-group)	gene	complement (4342. .4808)
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REFERENCE	1	CDS	/note="supported by full-length cDNA (s) : AK058832"
AUTHORS	Sasaki, T., Matsumoto, T. and Yamamoto, K.		complement (4442. .4759)
TITLE	Oryza sativa nipponbare (G33) genomic DNA, chromosome 2, PAC clone: P0431B06		/gene="P0431B06.2"
JOURNAL	Published Only in Database (2002)		/note="contains full-length cDNA (s) : AK058832"
REFERENCE	2 (bases 1 to 154796)		/codon_start=1
AUTHORS	Sasaki, T., Matsumoto, T. and Yamamoto, K.		/product="unknown protein"
JOURNAL	Direct Submission		/protein_id="BAD15627.1"
	Submitted (20-FEB-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannonnai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan		/db_xref="GI:46390196"
	(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/, Tel: 81-298-38-7441, Fax: 81-298-38-7468)		/translation="MKVKAVLVGRPREREREGCVRRRREGGRRAPDPARGRVVGR RIGVGVRLLDPASRPPEGAAVRGGARRRPRAVAHTCRCLPLPSPSMPATASMAG IEE"
COMMENT	On Apr 14, 2004 this sequence version replaced gi:33468820. Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://www.tigr.org/cdb/glimmer/glmr form.html), RiceHMM (http://rgp.dna.affrc.go.jp/RiceHMM/), _SplicePredictor (http://bioinformatics.lasstate.edu/cgi-bin/sp.cgi), sim4 (http://globin.cse.psu.edu/html/docs/sim4.html), gap2 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologues of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from T7 to SP6 of the PAC clone. This sequence of P0431B06 clone has an overlap with OSJNBa0078N11 (DDBJ: AP005848) clone at 5' end and with OJL288 G09 (DDBJ: AP004119) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html. Location/Qualifiers		complement (6499. .7930)
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Best Local Similarity 86.4%; Pred. No. 1.1e-15;
Matches 133; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 678 ATTAACGTGGAGATATAGAGAGGGGCTATCTGTTGGTTAGATGTGCCTTGGATGCT 737
Db 2393 ATTATCAGGAATACATAGAGAGGGGCTATCTGTTGGTTAGATGTGCCTTGGACGCT 2452
Qy 738 CTTGCTAGGCGTATGCTAAGTGGGAACGCTCTCGCTCTCTCTGGACCAACCATCT 797
Db 2453 CTTGCTAGGCGTATGCTAAGTGGGACGCTCGCTCTCTCTCTAGATCAACCATCT 2512
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Db 2513 GGTGATCCATACACATGGTGACTACTTGGCCCA 2546

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Search completed: August 25, 2005, 19:08:32
Job time : 5411 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2005, 12:54:01 ; Search time 726 Seconds
(without alignments)
9784.696 Million cell updates/sec

Title: US-10-660-226-9
Perfect score: 1200
Sequence: 1 ccgccaccagctacctgcc.....aaaaaaaaaaaaaaaaaaaa 1200

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues 8780412
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: Geneseqn1980s:*
 - 2: Geneseqn1990s:*
 - 3: Geneseqn2000s:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
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 - 9: Geneseqn2003bs:*
 - 10: Geneseqn2003cs:*
 - 11: Geneseqn2003ds:*
 - 12: Geneseqn2004as:*
 - 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	239.4	20.0	912	3 AAC50023	Aac50023 Arabidops
2	236.8	19.7	1365	3 AAC50026	Aac50026 Arabidops
3	236.8	19.7	1491	3 AAC50029	Aac50029 Arabidops
4	236.2	19.7	1363	3 AAC36026	Aac36026 Arabidops
5	233.6	19.5	637	10 ADK52674	Adk52674 Plant DNA
6	227	18.9	1484	3 AAC40184	Aac40184 Arabidops
7	188.4	15.7	1095	3 AAC47100	Aac47100 Arabidops
8	181	15.1	1093	3 AAC36746	Aac36746 Arabidops
9	166.6	13.9	660	3 AAC41622	Aac41622 Arabidops
10	163	13.6	660	10 ADK58257	Adk58257 Plant DNA
11	157	13.1	309	6 ABN79354	Abn79354 Human kin
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14	130	10.8	1010	13 ADR60835	Adr60835 Cotton cd
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17	94.6	7.9	537	10 ADK58256	Adk58256 Plant DNA
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19	82.6	6.9	255	7 ADK66821	Adk66821 Corn seed
20	79.4	6.6	402	13 ADT44359	Adt44359 Bacterial

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24	60.2	5.0	1479	13	ADS48191	Ad848191 Bacterial
25	59.2	4.9	507	13	ADS45422	Ad845422 Bacterial
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ALIGNMENTS

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XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 63305.
XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway; metabolic pathway;
XX KW promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
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PR 17-JUN-1999; 99US-0139492P. PR 13-AUG-1999; 99US-0148684P.
PR 18-JUN-1999; 99US-0139454P. PR 16-AUG-1999; 99US-0149368P.
PR 18-JUN-1999; 99US-0139455P. PR 17-AUG-1999; 99US-0149175P.
PR 18-JUN-1999; 99US-0139456P. PR 18-AUG-1999; 99US-0149426P.
PR 18-JUN-1999; 99US-0139457P. PR 20-AUG-1999; 99US-0149722P.
PR 18-JUN-1999; 99US-0139458P. PR 20-AUG-1999; 99US-0149723P.
PR 18-JUN-1999; 99US-0139459P. PR 20-AUG-1999; 99US-0149929P.
PR 18-JUN-1999; 99US-0139460P. PR 20-AUG-1999; 99US-0149902P.
PR 18-JUN-1999; 99US-0139461P. PR 23-AUG-1999; 99US-0149930P.
PR 18-JUN-1999; 99US-0139462P. PR 25-AUG-1999; 99US-0150566P.
PR 18-JUN-1999; 99US-0139463P. PR 26-AUG-1999; 99US-0150884P.
PR 18-JUN-1999; 99US-0139750P. PR 27-AUG-1999; 99US-0151065P.
PR 18-JUN-1999; 99US-0139763P. PR 27-AUG-1999; 99US-0151066P.
PR 21-JUN-1999; 99US-0139817P. PR 27-AUG-1999; 99US-0151080P.
PR 22-JUN-1999; 99US-0139899P. PR 30-AUG-1999; 99US-0151303P.
PR 23-JUN-1999; 99US-0140353P. PR 31-AUG-1999; 99US-0151438P.
PR 23-JUN-1999; 99US-0140354P. PR 01-SEP-1999; 99US-0151930P.
PR 24-JUN-1999; 99US-0140695P. PR 07-SEP-1999; 99US-0152363P.
PR 28-JUN-1999; 99US-0140823P. PR 10-SEP-1999; 99US-0153070P.
PR 28-JUN-1999; 99US-0140991P. PR 13-SEP-1999; 99US-0153758P.
PR 30-JUN-1999; 99US-0141287P. PR 15-SEP-1999; 99US-0154018P.
PR 01-JUL-1999; 99US-0141842P. PR 16-SEP-1999; 99US-0154039P.
PR 01-JUL-1999; 99US-0142154P. PR 20-SEP-1999; 99US-0154779P.
PR 02-JUL-1999; 99US-0142055P. PR 22-SEP-1999; 99US-0155139P.
PR 06-JUL-1999; 99US-0142390P. PR 23-SEP-1999; 99US-0155486P.
PR 08-JUL-1999; 99US-0142803P. PR 24-SEP-1999; 99US-0155659P.
PR 09-JUL-1999; 99US-0142820P. PR 28-SEP-1999; 99US-0156458P.
PR 12-JUL-1999; 99US-0142977P. PR 29-SEP-1999; 99US-0156596P.
PR 13-JUL-1999; 99US-0143542P. PR 04-OCT-1999; 99US-0157117P.
PR 14-JUL-1999; 99US-0143624P. PR 05-OCT-1999; 99US-0157753P.
PR 15-JUL-1999; 99US-0144005P. PR 06-OCT-1999; 99US-0157865P.
PR 16-JUL-1999; 99US-0144086P. PR 07-OCT-1999; 99US-0158029P.
PR 19-JUL-1999; 99US-0144325P. PR 08-OCT-1999; 99US-0158232P.
PR 19-JUL-1999; 99US-0144331P. PR 12-OCT-1999; 99US-0158369P.
PR 19-JUL-1999; 99US-0144332P. PR 13-OCT-1999; 99US-0159293P.
PR 19-JUL-1999; 99US-0144333P. PR 13-OCT-1999; 99US-0159294P.
PR 19-JUL-1999; 99US-0144334P. PR 13-OCT-1999; 99US-0159295P.
PR 19-JUL-1999; 99US-0144335P. PR 14-OCT-1999; 99US-0159329P.
PR 20-JUL-1999; 99US-0144352P. PR 14-OCT-1999; 99US-0159330P.
PR 20-JUL-1999; 99US-0144632P. PR 14-OCT-1999; 99US-0159331P.
PR 20-JUL-1999; 99US-0144684P. PR 14-OCT-1999; 99US-0159637P.
PR 21-JUL-1999; 99US-0144814P. PR 18-OCT-1999; 99US-0159584P.
PR 21-JUL-1999; 99US-0145086P. PR 21-OCT-1999; 99US-0160741P.
PR 21-JUL-1999; 99US-0145088P. PR 21-OCT-1999; 99US-0160767P.
PR 22-JUL-1999; 99US-0145085P. PR 21-OCT-1999; 99US-0160768P.
PR 22-JUL-1999; 99US-0145087P. PR 21-OCT-1999; 99US-0160770P.
PR 22-JUL-1999; 99US-0145089P. PR 21-OCT-1999; 99US-0160814P.
PR 22-JUL-1999; 99US-0145192P. PR 21-OCT-1999; 99US-0160815P.

	22-OCT-1999;	99US-0160980P.		20.0%;	Score 239.4;	DB 3;	Length 912;	
	22-OCT-1999;	99US-0160981P.		Best Local Similarity	62.4%;	Pred. No. 1.9e-45;		
	22-OCT-1999;	99US-0160989P.		Matches 375;	Conservative 0;	Mismatches 226;	Indels 0;	Gaps 0;
Qy	382	TGAAGAGAAATCAGAAGATTCTGTTCTACTTGAACGGGAGGTGTATTTACTCTAGTAG 441						
Db	266	TCAAGAGAAAGCAGAAGAGGTTAAACCGTATTGTAATGGACGACTCTATGTACCTTTGTCTG 325						
Qy	442	GAATGATGGGTTCTGGAAAACTACTGTGGGGAAGATTATGTCTGAAGTCTCTGGGTATT 501						
Db	326	GAATGATGGGTTCTGGAAAACTACTGTGGGAAAAGTTAATGTGCCAAGTGTCTCGGTTATA 385						
Qy	502	CGTTCTTTCATAGTCACAAGTTAGTGGAGCAAGCTGTGGAAATGCCATCAGTTGCCCAA 561						
Db	386	CGTTCTTTCATAGTCGGACACTTTGATGAAACAGGCCGATGAATGGAACTTCTGTTGCAGAGA 445						
Qy	562	TATTCAAAGTCCATAGTGAAGCCTTCTTTCCGGGATAATGAGAGTAGTGTCTTCGAGAGATT 621						
Db	446	TATTTGTTTCATCAGCGAGAGATTCTTTTAGAGGAAAGGAGACCGATGCGCTTTAAGAAGC 505						
Qy	622	TGTCCTCCATGCGACGATTAGTTGTGCCACCGGAGGTGGTCTGTTTATCCGACCAATTA 581						
Db	506	TCTCTTCGAGGTATCAAGTTGTGTTTCCACAGGTGGAGGTGCAGTTTATGAAGACCCATTA 565						
Qy	682	ACTGGAGATATATGAAGAGGGGCCCTATCTGTTTGGTTAGATGTGCCCTTCGATGCTCTTG 741						
Db	566	ACTGGAAGTATATGCATAAAGAAATCAGCATTTGGCTAGATGTGCTCTAGAGACATTAG 525						
Qy	742	CTAGGCGTATATGCTAAAGTGGGAACTGCCTCTCGTCTCTTCTGGACCAACCACTCTGGTG 801						
Db	626	CCCATAGAAATCGCTGCTGTTGGAACCTGATTCAACGACCACCTGCTACACGATGAATCAGGAG 585						
Qy	802	ATCCGTACCGAATGGCCCTTTCTAAGCTCAGCATGCTTGACACAGAAAGGGGTGATGCTT 861						
Db	686	ATGCATACTCAGTGGGCTTTCAAACGCTCTCTCGGCTATTTTGGGACGACGGCGGTGAAGCAT 745						
Qy	862	ATGCAAAATCAGATGTAAGGGTTTCTCTGGGAAGAGATTGCATGTAACAAAGGTCATGATG 921						
Db	746	ACAAACCGAAATGCCAGTCTCTTAGAAAATATTTCGAGCAACGCGTGGCTATTAA 805						
Qy	922	ATGTCTCTAAGCTGCACCTACTCTGATATTGCAATTGAGTCACTTTCATAAGATCGAGAGCT 981						
Db	806	ATGTCTCAGATCTCACCACTGAAATGCTATCGAGGCCCTTCGACCAAGTTCTGAGCT 865						
Qy	982	T 982						
Db	866	T 866						

RESULT 2	
AAC50026	
ID	AAC50026 standard; DNA; 1365 BP.
XX	
XX	
XX	
XX	
DT	18-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana DNA fragment
XX	

PR	23-JUN-1999;	99US-0140354P.	PR	01-SEP-1999;	99US-0151930P.
PR	24-JUN-1999;	99US-0140695P.	PR	07-SEP-1999;	99US-0152363P.
PR	26-JUN-1999;	99US-0140823P.	PR	10-SEP-1999;	99US-0153070P.
PR	29-JUN-1999;	99US-0140991P.	PR	13-SEP-1999;	99US-0153758P.
PR	30-JUN-1999;	99US-0141184P.	PR	15-SEP-1999;	99US-0154018P.
PR	01-JUL-1999;	99US-0141842P.	PR	16-SEP-1999;	99US-0154039P.
PR	01-JUL-1999;	99US-0142154P.	PR	20-SEP-1999;	99US-0154779P.
PR	02-JUL-1999;	99US-0142055P.	PR	22-SEP-1999;	99US-0155139P.
PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-0155486P.
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.
PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0143277P.	PR	29-SEP-1999;	99US-0156596P.
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157753P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144884P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0144814P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161992P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
PR	04-AUG-1999;	99US-0147302P.	Query Match		
PR	05-AUG-1999;	99US-0147192P.	Best Local Similarity		
PR	05-AUG-1999;	99US-0147260P.	Score 236.8; DB 3; Length 1365;		
PR	06-AUG-1999;	99US-0147303P.	Pred. No. 8.7e-45;		
PR	06-AUG-1999;	99US-0147416P.	Matches 373; Conservative		
PR	09-AUG-1999;	99US-0147493P.	0; Mismatches 227; Indels		
PR	09-AUG-1999;	99US-0147935P.	0; Gaps		
PR	10-AUG-1999;	99US-0148171P.	0;		
PR	11-AUG-1999;	99US-0148319P.	QY	383	GAAGAGAAATCAGAAGATTCTTCTTACTTGAACGGAGGTCTATTACCTAGTAGG 442
PR	12-AUG-1999;	99US-0148341P.	DB	377	GCAAGAAAGCAGAAGAGGTTAAACCGTATTTGAATGGACGATCTATGTACTCTTTCGG 436
PR	13-AUG-1999;	99US-0148565P.	QY	443	AATGATGGTCTCTGGAAGAAAGTACTGTGGGAAGATTATGTCTGAAGTCTTCGGTTATTC 502
PR	13-AUG-1999;	99US-0148684P.	DB	437	AATGATGGTCTCTGGAAGAAACAACTGTGGGAAGTTAATGTCCAAGTCTCGGTTATAC 496
PR	16-AUG-1999;	99US-0149368P.	QY	503	GTTCTTTGATAGTGAACAAGTTAGTGGAGCAAGCTCTTTGGAAATGCCATCAGTTGCCAAAT 562
PR	17-AUG-1999;	99US-0149175P.	DB	497	GTTCTTTGACTCGGACACTTTTGATTGAACAGGCGATGAATGGAACTTCTGTTGCAGAGAT 556
PR	20-AUG-1999;	99US-0149723P.	QY	563	ATTCAAGGTCCATAGTAGTGAAGCCCTTTTCGGGATATAGAGATAGTGTTCGAGAGATTT 622
PR	20-AUG-1999;	99US-0149929P.	DB	557	ATTTGTTTCATCACGGAGAGAAATTTTTTAGAGNAAAGGAGACCGATGCGCTTTAAGAAGCT 616
PR	23-AUG-1999;	99US-0149930P.	QY	623	GTCCTCCATCGACGATTAGTTGTCACCGAGGTGGTGTCTGTATCCGACCAATTAA 682
PR	25-AUG-1999;	99US-0150566P.	DB	617	CTCTTCGAGGTATCAAGTTGTTGTTTCCACAGTGGAGGTGCAGTTATAAGACCCATTAA 676
PR	26-AUG-1999;	99US-0150884P.	QY	683	CTGGAGATATATGAAGAGGGGCCTATCTGTTTGGTTAGATGTGCCCTTGGATGCTCTTCG 742
PR	27-AUG-1999;	99US-0151065P.			
PR	27-AUG-1999;	99US-0151066P.			
PR	30-AUG-1999;	99US-0151080P.			
PR	30-AUG-1999;	99US-0151303P.			
PR	31-AUG-1999;	99US-0151438P.			

Db	677	CTGGAAGTATATGCATAAAGGAATCAGCAATTTGGCTAGATGCGCTCTAGAGCATTAGC	736	PR	25-MAY-1999;	99US-0136021P.
Qy	743	TAGGCGTATTGTCTAAAGTGGGAACCTGCCTCTCGTCTCTTTCTGGACCAACCATCTGGTCA	802	PR	27-MAY-1999;	99US-0136392P.
Db	737	CCATAGAATCGCTGCTGTTGGAACTGATTCACGACCACTGCTACACGATGAATCAGGAGA	796	PR	28-MAY-1999;	99US-0136782P.
Qy	803	TCCGTACGGAATGGCGCTTTTCTAAGCTCAGCATGCTTGCACAGCAAGGGGTGATGCTTA	862	PR	01-JUN-1999;	99US-0137222P.
Db	797	TGCATACTCAGTGGCTTTCAAACGCTCTCTCGGCTATTGGGACGAGCGGCTGAAGCATA	856	PR	03-JUN-1999;	99US-0137528P.
Qy	863	TGCAAAATGCAGATGTAAGGTTTCTCTGGAAGAGATTGCATGTAACAAGGTCATGATCA	922	PR	04-JUN-1999;	99US-0137502P.
Db	857	CACAAACGGAATGCCAGAGTCTCTTAGAAAATATTGCAGCAAAAGCGTGGCTATATAAAA	916	PR	07-JUN-1999;	99US-0137724P.
Qy	923	TGTCTCTAAGCTGACACCTACTACTGATATTGCAATTGAGTCACATTTCATAAGATCGAGAGCTT	982	PR	08-JUN-1999;	99US-0138094P.
Db	917	TGTCTCAGATCTCACACCACTGAAATTTGCTATCGAGGCTTCGACCAAGTTCTGAGCTT	976	PR	10-JUN-1999;	99US-0138540P.
RESULT 3						
AAC50029						
ID	AAC50029 standard; DNA; 1491 BP.					
XX	AAC50029;					
AC						
XX						
DT	18-OCT-2000 (first entry)					
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 63328.					
DE						
XX						
KW	Hybridisation assay; genetic mapping; gene expression control;					
KW	protein identification; signal transduction pathway; metabolic pathway;					
*KW	promoter; termination sequence; ss.					
OS	Arabidopsis thaliana.					
XX						
PN	EP1033405-A2.					
XX						
PD	06-SEP-2000.					
XX						
XX	25-FEB-2000; 2000EP-00301439.					
PR	25-FEB-1999;	99US-0121825P.		PR	12-JUL-1999;	99US-0142977P.
PR	05-MAR-1999;	99US-0123180P.		PR	13-JUL-1999;	99US-0143542P.
PR	09-MAR-1999;	99US-0123548P.		PR	14-JUL-1999;	99US-0143624P.
PR	23-MAR-1999;	99US-0125788P.		PR	15-JUL-1999;	99US-0144005P.
PR	25-MAR-1999;	99US-0126264P.		PR	16-JUL-1999;	99US-0144085P.
PR	29-MAR-1999;	99US-0126785P.		PR	16-JUL-1999;	99US-0144086P.
PR	01-APR-1999;	99US-0127462P.		PR	19-JUL-1999;	99US-0144325P.
PR	06-APR-1999;	99US-0128234P.		PR	19-JUL-1999;	99US-0144331P.
PR	08-APR-1999;	99US-0128714P.		PR	19-JUL-1999;	99US-0144332P.
PR	16-APR-1999;	99US-0129845P.		PR	19-JUL-1999;	99US-0144333P.
PR	19-APR-1999;	99US-0130077P.		PR	19-JUL-1999;	99US-0144334P.
PR	21-APR-1999;	99US-0130449P.		PR	20-JUL-1999;	99US-0144335P.
PR	23-APR-1999;	99US-0130510P.		PR	20-JUL-1999;	99US-0144632P.
PR	23-APR-1999;	99US-0130891P.		PR	20-JUL-1999;	99US-0144884P.
PR	28-APR-1999;	99US-0131449P.		PR	21-JUL-1999;	99US-0144814P.
PR	30-APR-1999;	99US-0132048P.		PR	21-JUL-1999;	99US-0145086P.
PR	30-APR-1999;	99US-0132407P.		PR	21-JUL-1999;	99US-0145088P.
PR	04-MAY-1999;	99US-0132484P.		PR	22-JUL-1999;	99US-0145085P.
PR	05-MAY-1999;	99US-0132485P.		PR	22-JUL-1999;	99US-0145087P.
PR	06-MAY-1999;	99US-0132486P.		PR	22-JUL-1999;	99US-0145089P.
PR	07-MAY-1999;	99US-0132487P.		PR	22-JUL-1999;	99US-0145192P.
PR	11-MAY-1999;	99US-0134256P.		PR	23-JUL-1999;	99US-0145145P.
PR	14-MAY-1999;	99US-0134218P.		PR	23-JUL-1999;	99US-0145218P.
PR	14-MAY-1999;	99US-0134219P.		PR	26-JUL-1999;	99US-0145224P.
PR	14-MAY-1999;	99US-0134221P.		PR	27-JUL-1999;	99US-0145276P.
PR	14-MAY-1999;	99US-0134370P.		PR	27-JUL-1999;	99US-0145913P.
PR	18-MAY-1999;	99US-0134768P.		PR	27-JUL-1999;	99US-0145918P.
PR	19-MAY-1999;	99US-0134941P.		PR	28-JUL-1999;	99US-0145951P.
PR	20-MAY-1999;	99US-0135124P.		PR	02-AUG-1999;	99US-0146386P.
PR	21-MAY-1999;	99US-0135353P.		PR	02-AUG-1999;	99US-0146388P.
PR	24-MAY-1999;	99US-0135629P.		PR	02-AUG-1999;	99US-0146389P.

PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
PR	04-AUG-1999;	99US-0147302P.		Query Match	19.7%; Score 236.8; DB 3; Length 1491;
PR	05-AUG-1999;	99US-0147192P.		Best Local Similarity	62.2%; Pred. No. 8.9e-45;
PR	05-AUG-1999;	99US-0147260P.		Matches 373; Conservative	0; Mismatches 227; Indels 0; Gaps 0;
PR	06-AUG-1999;	99US-0147303P.			
PR	06-AUG-1999;	99US-0147416P.	QY	383	GAAGAGAAATCAGAAGAGTTCTGTTCTACTTGAACGGGAGGTGTTATTTACCTAGTAGG 442
PR	09-AUG-1999;	99US-0147493P.	Db	551	GCAAGAAAGCAGAGAGGTTAAACCGTATTTCGAATGGACGATCTATGTACCTTGTTCGG 610
PR	09-AUG-1999;	99US-0147935P.			
PR	10-AUG-1999;	99US-0148171P.	QY	443	AATGATGGGTTCTGSAAAAAGTACTGTGGGGAAGATTATGTCGAAGCTTTGGGTTATTC 502
PR	11-AUG-1999;	99US-0148319P.	Db	611	AATGATGGGTTCTGGAAAAACAACGTGGGAAAGTTAATGTCCAAAGTGTCTCGGTTATAC 670
PR	12-AUG-1999;	99US-0148341P.			
PR	13-AUG-1999;	99US-0148565P.	QY	503	GTTCTTTCATAGTGACAGTTAGTGGAGCAAGCTGTTGGAAATGCCATCAGTTCGCCAAAT 562
PR	16-AUG-1999;	99US-0149368P.	Db	671	GTTCTTTCAGCTGGGACACTTTGATTTGAACACAGCGCATGAATGGAACTTCTGTTGAGAGAT 730
PR	17-AUG-1999;	99US-0149175P.			
PR	18-AUG-1999;	99US-0149426P.	QY	563	ATTCAAGGTCATAGTGAAGCCTTCTTTCCGGATAAATCAGAGTAGTGTCTTTGAGAGATTT 622
PR	20-AUG-1999;	99US-0149722P.	Db	731	ATTTGTTTCATCACGGAGAGAAATTTTTTAGAGGAAGAGAGACCGATCGGCTTAAGAAGCT 790
PR	20-AUG-1999;	99US-0149723P.			
PR	23-AUG-1999;	99US-0149929P.	QY	623	GTCTCCATGCGACGATTAGTTGTGCGCACCGGAGGTGGTGTGTTATCCGACCAATTAA 682
PR	23-AUG-1999;	99US-0149930P.	Db	791	CTCTTCGAGGTATCAAGTTGTTGTTTCCACAGGTGGAGGTGCAGTTATAAGACCCATTAA 850
PR	25-AUG-1999;	99US-0150566P.			
PR	26-AUG-1999;	99US-0150884P.	QY	683	CTGGAGATATATGAGAGGGGCCCTATCTGTTTGGTTAGATGTGCCCTTGGATGCTCTTGC 742
PR	27-AUG-1999;	99US-0151066P.	Db	851	CTGGAAGTATATGTCATAAAGGAATCAGCAITTTGGCTAGATGTGCTCTTAGAAGCATTTAGC 910
PR	27-AUG-1999;	99US-0151080P.			
PR	30-AUG-1999;	99US-0151303P.	QY	743	TAGGCGTATTGCTAAAGTGGGAACTGCTCTCGTCTCTCTTCTTGACCAACCATCTGTGTGA 802
PR	31-AUG-1999;	99US-0151438P.	Db	911	CCATAGAAATCGCTGCTGTTGGAACTGATTACGACCACTGCTACACGATGAATCAGGAGA 970
PR	01-SEP-1999;	99US-0151930P.			
PR	07-SEP-1999;	99US-0152363P.	QY	803	TCCGTACGCAATGGCCTTTTCTAAGCTCAGCATGCTTGCACAGCAAAAGGGGTGATGCTTA 862
PR	10-SEP-1999;	99US-0153070P.	Db	971	TGCATACTCAGTGGCTTTCAAACGCTCTCTCGGCTATTTTGGGAACGAGCGGTGAAGCATTA 1030
PR	13-SEP-1999;	99US-0153758P.			
PR	15-SEP-1999;	99US-0154018P.	QY	863	TGCAAAATGCAGATGTAAGGGTTTCTCTGGAAGAGATTGCAATGTAACAAGTCAATGATGA 922
PR	16-SEP-1999;	99US-0154039P.	Db	1031	CACAAACGCAATGCCAGAGTCTCCTTAGAAAAATTTGCAGCAAAAGCGTGGCTATATAAAA 1090
PR	20-SEP-1999;	99US-0154779P.			
PR	22-SEP-1999;	99US-0155139P.	QY	923	TGTCTCTAAGCTGCACACCTACTGATATTTGCAATTGAGTCACTTCATAAGATCGAGAGCTT 982
PR	23-SEP-1999;	99US-0155486P.	Db	1091	TGTCTCAGATCTCACACCAACTGAAATTGCTATCGAGGCCTTCGAGCAAGTTCGTGACTT 1150
PR	24-SEP-1999;	99US-0155659P.			
PR	28-SEP-1999;	99US-0156458P.		RESULT 4	
PR	29-SEP-1999;	99US-0156596P.		AAC36026	
PR	04-OCT-1999;	99US-0157117P.	ID	AAC36026 standard; DNA; 1363 BP.	
PR	05-OCT-1999;	99US-0157753P.	XX	AAC36026;	
PR	06-OCT-1999;	99US-0157865P.	AC	AAC36026;	
PR	07-OCT-1999;	99US-0158029P.	XX		
PR	08-OCT-1999;	99US-0158232P.	DT	17-OCT-2000 (first entry)	
PR	12-OCT-1999;	99US-0158369P.	XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 12278.	
PR	13-OCT-1999;	99US-0159293P.	DE	Arabidopsis thaliana.	
PR	13-OCT-1999;	99US-0159294P.	XX		
PR	13-OCT-1999;	99US-0159295P.	KW	Hybridisation assay; genetic mapping; gene expression control;	
PR	14-OCT-1999;	99US-0159329P.	KW	protein identification; signal transduction pathway; metabolic pathway;	
PR	14-OCT-1999;	99US-0159330P.	KW	promoter; termination sequence; ss.	
PR	14-OCT-1999;	99US-0159331P.	XX		
PR	14-OCT-1999;	99US-0159637P.	XX	Arabidopsis thaliana.	
PR	14-OCT-1999;	99US-0159638P.	XX		
PR	18-OCT-1999;	99US-0159584P.	PN	EP1033405-A2.	
PR	21-OCT-1999;	99US-0160741P.	XX		
PR	21-OCT-1999;	99US-0160767P.	PD	06-SEP-2000.	
PR	21-OCT-1999;	99US-0160768P.	XX		
PR	21-OCT-1999;	99US-0160770P.	PF	25-FEB-2000; 2000EP-00301439.	
PR	21-OCT-1999;	99US-0160814P.	XX		
PR	21-OCT-1999;	99US-0160815P.	PR	25-FEB-1999; 99US-0121825P.	
PR	22-OCT-1999;	99US-0160980P.	PR	05-MAR-1999; 99US-0123180P.	
PR	22-OCT-1999;	99US-0160980P.	PR	09-MAR-1999; 99US-0123548P.	
PR	22-OCT-1999;	99US-0160981P.			
PR	22-OCT-1999;	99US-0160989P.			
PR	25-OCT-1999;	99US-0161404P.			
PR	25-OCT-1999;	99US-0161405P.			
PR	25-OCT-1999;	99US-0161406P.			
PR	26-OCT-1999;	99US-0161359P.			
PR	26-OCT-1999;	99US-0161360P.			
PR	26-OCT-1999;	99US-0161361P.			
PR	28-OCT-1999;	99US-0161920P.			
PR	28-OCT-1999;	99US-0161922P.			

PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131144P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
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PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-01334256P.
PR 14-MAY-1999; 99US-0134218P.
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PR 19-MAY-1999; 99US-0134941P.
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PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137522P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
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PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142290P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143442P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.

PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
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PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145911P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
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PR 17-AUG-1999; 99US-0149175P.
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PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.

PR	07-OCT-1999;	99US-0158029P.	
PR	08-OCT-1999;	99US-0158232P.	
PR	12-OCT-1999;	99US-0158369P.	
PR	13-OCT-1999;	99US-0159293P.	
PR	13-OCT-1999;	99US-0159294P.	
PR	13-OCT-1999;	99US-0159295P.	
PR	14-OCT-1999;	99US-0159329P.	
PR	14-OCT-1999;	99US-0159330P.	
PR	14-OCT-1999;	99US-0159331P.	
PR	14-OCT-1999;	99US-0159637P.	
PR	14-OCT-1999;	99US-0159638P.	
PR	18-OCT-1999;	99US-0159584P.	
PR	21-OCT-1999;	99US-0160741P.	
PR	21-OCT-1999;	99US-0160767P.	
PR	21-OCT-1999;	99US-0160768P.	
PR	21-OCT-1999;	99US-0160770P.	
PR	21-OCT-1999;	99US-0160814P.	
PR	21-OCT-1999;	99US-0160815P.	
PR	22-OCT-1999;	99US-0160980P.	
PR	22-OCT-1999;	99US-0160981P.	
PR	22-OCT-1999;	99US-0160989P.	
PR	25-OCT-1999;	99US-0161404P.	
PR	25-OCT-1999;	99US-0161405P.	
PR	25-OCT-1999;	99US-0161406P.	
PR	26-OCT-1999;	99US-0161359P.	
PR	26-OCT-1999;	99US-0161360P.	
PR	26-OCT-1999;	99US-0161361P.	
PR	28-OCT-1999;	99US-0161920P.	
PR	28-OCT-1999;	99US-0161992P.	
PR	28-OCT-1999;	99US-0161993P.	
PR	29-OCT-1999;	99US-0162142P.	
Query Match 19.7%; Score 236.2; DB 3; Length 1363;			
Best Local Similarity 62.1%; Pred. No. 1.2e-44;			
Matches 373; Conservative 0; Mismatches 228; Indels 0; Gaps 0;			
QY	382	TGAAGAGAAATCAGAGAAGTCTCTTCTACTTTGAACGGAGGTGTTATTTACCTAGTAG	441
DB	372	TCAGAGAAAGCAGAGAAGGTTAAACCGTATTTGAATGGACGATCTATGTCCTTGTG	431
QY	442	GAATGATGGTTCTGGAAAAAGTACTGTGGGAAGATTATGTCGAACTCTTGGGTTATT	501
DB	432	GAATGATGGTTCTGGAAAAACAACTGTGGAAAGTTAATGTCCAAAGTCTCGGTTATA	491
QY	502	CGTCTTTCATGACGAGTTAGTGGACGACGCTGTTGGAATGCCATCAGTTGCCCAA	561
DB	492	CGTCTTTCATGACGAGTTAGTGGACGACGCTGTTGGAATGCCATCAGTTGCCCAA	551
QY	562	TATTCAGGTCCTAGTGAAGCCTTCTTTCGGGATTAATGAGAGTAGTGTCTTGAGAGATT	621
DB	552	TATTTGTTTCATCAGGAGAGATTTTTTTAGAGAAAGGAGACCGATCGCTTNAAGC	611
QY	622	TGTCCTCCATGCGAAGATTAGTTGTTGCCACCGAGGTGGTGTCTGTTATCCGACCAATTA	681
DB	612	TCTCTTCGAGGTATCAAGTTGTTGTTTCCACAGGTGGAGTGCAGTTATAAGACCCATTA	671
QY	682	ACTGGAGATATGAGAGGGGCTATCTGTTGGTTAGATGTCGCCCTTGGATGCTCTTG	741
DB	672	ACTGGAAGTATATGCAATGAAGGAATCAGCATTTTGGCTAGATGTCCTAGAAAGCATTAG	731
QY	742	CTAGGCGTATTGCTAAAGTGGGAACCTCTCGTCTCTTCTGGACCAACCATCTGCTG	801
DB	732	CCCATAGATTCGCTGCTGTTGGAACTGATTCAGACCACTGCTACAGATGATCAGGAG	791
QY	802	ATCCGTACGCAATGGCCTTTTCTTAAGCTCAGCATGCTTGCACAGCAAAAGGGTGATG	861
DB	792	ATGCATACTCAGTGGCTTTTCAACAGCTCTCTCGGCTATTGTTGGACGACGCGGTGAAGCAT	851
QY	862	ATCCAAATCAGATTAAGGTTTCTCTGGAAGATTCGATGTAAACAGGTCATGATG	921
DB	852	ACAAACCGCAATGCCAGAGTCTCTCTTAGAAATATTGCAGCAAAAGCGTGGCTATAAA	911
QY	922	ATGTCCTTAAGCTGACACCTACTACTATATTGCAATTGAGTCACTTTCATAAGATCGAGCT	981

Db	912	ATGCTCAGATCTCACCAACTGAATTTGTATCGAGGCTTCGAGCAAGTCTTGAGCT	971
QY	982	T 982	
Db	972	T 972	
RESULT 5			
ID	ADKS2674	standard; DNA; 637 BP.	
XX	ADKS2674;		
XX	06-MAY-2004	(first entry)	
XX	Plant DNA sequence which confers altered metabolic characteristic #57.		
XX	altered metabolic characteristic; plant; acid metabolism;		
KW	alcohol metabolism; fatty acid metabolism;		
KW	branched fatty acid metabolism; alkaloid metabolism;		
KW	amino acid metabolism; ester metabolism; glyceride metabolism;		
KW	phenolic metabolism; carbohydrate metabolism; steroid metabolism;		
KW	terpene metabolism; isoprenoid metabolism; alkene metabolism;		
KW	alkyne metabolism; hydrocarbon metabolism; ketone metabolism;		
KW	quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.		
XX	Nicotiana benthamiana.		
OS	WO2003020936-A1.		
PN	13-MAR-2003.		
XX	30-AUG-2002; 2002WO-US027884.		
XX	31-AUG-2001; 2001US-0316471P.		
XX	(DOWC) DOW CHEM CO.		
XX	(DOWC) DOW AGROSCIENCES LLC.		
PA	Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;		
PI	Oriado JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;		
PI	WPI; 2003-313091/30.		
DR	Novel genes that confer altered metabolic characteristics in Nicotiana		
XX	benthamiana plants, useful for altering the levels of metabolites e.g.		
PT	acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.		
XX	Claim 1; SEQ ID NO 57; 2576pp; English.		
XX	The invention comprises DNA sequences which confer an altered metabolic		
CC	characteristic when they are expressed in a plant. The DNA sequences of		
CC	the invention are useful for producing plants with an altered metabolic		
CC	characteristic, such as: altered acid metabolism, alcohol metabolism,		
CC	fatty acid metabolism, branched fatty acid metabolism, alkaloid or other		
CC	base metabolism, altered amino acid metabolism, altered ester metabolism,		
CC	altered glyceride metabolism, altered phenolic metabolism, altered		
CC	carbohydrate metabolism, altered steroid, oxygenated terpene, or		
CC	isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon		
CC	metabolism, ketone or quinone metabolism. The DNA sequences of the		
CC	invention may be used to provide disease resistance in a plant and gene		
CC	shuffling or sexual PCR procedures. The present nucleic acid represents a		
CC	DNA sequence of the invention.		
XX	Sequence 637 BP; 185 A; 103 C; 165 G; 184 T; 0 U; 0 Other;		
XX	Query Match 19.5%; Score 233.6; DB 10; Length 637;		
XX	Best Local Similarity 63.7%; Pred. No. 3.8e-44;		
XX	Matches 372; Conservative 0; Mismatches 209; Indels 3; Gaps 1;		
QY	411	TACTTGAACGGAGGTGTTATTTACCTAGTAGGAATGATGGTCTCGAAAAAGTACTGTG	470

Db	9	TATCTAGATGGACGATGTATATACCTCGTTGGAGTGATGGCTCTGCGCAAAACAACCTGTG	68	PR	23-APR-1999;	99US-0130510P.
Qy	471	GGGAAGATTATGTCTGAAGCTTTGGGTTATTCGTTCTTTTCATAGTACAAAGTTAGTGGAG	530	PR	28-APR-1999;	99US-0130891P.
Db	69	GGCGTATTTTGGCAGAAACACTGGGATATTCCTTTTTCGACTGTGACAGGCTGATAGAG	128	PR	30-APR-1999;	99US-0132048P.
Qy	531	CAAGCTGTTGGATGCCATCAGTTGGTCCCAAAATTTCAAGTCCATAGTGAAGCCTTCTTTT	590	PR	04-MAY-1999;	99US-0132407P.
Db	129	CAGGCTGTTGGTGGAACTACAGTAGCTGAAATCTTCAAGCTTCGTGGAGAGAGCTTCTTTT	188	PR	05-MAY-1999;	99US-0132484P.
Qy	591	CGGGAATAACAGAGTAGTGTCTTGAGAGATTTGTCCTCCATCGAGCATTTAGTTGTTGCC	650	PR	06-MAY-1999;	99US-0132485P.
Db	189	AGGACAAATGAGACGGAGGTATTGCACAGCTGTCTGCGATGCATCGCTTGTGTGTTCA	248	PR	07-MAY-1999;	99US-0132486P.
Qy	651	ACCGAGGTGGTGTCTGTTATCCGACCAATTAACCTGGAGATATATGAAGAGGGGCCCTATCT	710	PR	11-MAY-1999;	99US-0132863P.
Db	249	ACAGGTGGAGTGCAGTTGTTGTCCTCCATTAATTGGAGACATATGCACAGGGTATTAGT	308	PR	14-MAY-1999;	99US-0134218P.
Qy	711	GTTTGGTTAGATGTGCCCTTGGATGCTCTTGCTAGGGGTATTGCTAAAGTGGGAACCTGCC	770	PR	14-MAY-1999;	99US-0134221P.
Db	309	GTTTGGTTAGATGTCTCTTTAGATGCTTTGGCCCAAGAGAGTTACTGCTGAAGGAACATAA	368	PR	18-MAY-1999;	99US-0134370P.
Qy	771	TCTCGTCTCTCTCTGGACCAACCATCTGGTGATCCGTAGCAATGSCCTTTTCTAAGCTC	830	PR	19-MAY-1999;	99US-0134768P.
Db	369	TCTCGACCCCTATTACATGAAGAAATCAGGAGACATTTATGTAAGACTTTGAAGCGGTTA	428	PR	20-MAY-1999;	99US-0134941P.
Qy	831	AGCATGCTTGCACAGCAAGGGGTGATGCTTATGCAAAATGCAGATGTAAAGGGTTTCTCTG	890	PR	21-MAY-1999;	99US-0135124P.
Db	429	ACTACTTAAATGAGACAGGGGTGAAAACTATGCCAATGCAAGTGTACGGGTTTTCACAT	488	PR	24-MAY-1999;	99US-0135353P.
Qy	891	GAAGAGATTGCATGTAAACAAGTGCATGATGATGCTCTTAAGCTGCACCTACTATATTT	950	PR	25-MAY-1999;	99US-0135629P.
Db	489	GAAATAATTTCAGTGAAGAGGGG---AAAAGATGCTGTGCCATATTACACCTACTGAAAT	545	PR	27-MAY-1999;	99US-0136021P.
Qy	951	GCAATTGAGTCATTCATAGATCGAGAGCTTCGTATCGAGCA	994	PR	28-MAY-1999;	99US-0136392P.
Db	546	ACTCTAGAGTTCTTATACAAATTCAGAACTTCTTAAAGAAACA	589	PR	01-JUN-1999;	99US-0136782P.
RESULT 6						
AAC40184						
ID	AAC40184 standard; DNA; 1484 BP.					
XX	AAC40184;					
XX	17-OCT-2000 (first entry)					
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 27368.					
XX	Hybridisation assay; genetic mapping; gene expression control;					
KW	protein identification; signal transduction pathway; metabolic pathway;					
KW	promoter; termination sequence; ss.					
XX	Arabidopsis thaliana.					
XX	EP1033405-A2.					
XX	06-SEP-2000.					
PF	25-FEB-2000; 2000EP-00301439.					
XX	25-FEB-1999; 99US-0121825P.					
PR	05-MAR-1999; 99US-0123180P.					
PR	09-MAR-1999; 99US-0123548P.					
PR	23-MAR-1999; 99US-0125788P.					
PR	25-MAR-1999; 99US-0126264P.					
PR	29-MAR-1999; 99US-0126785P.					
PR	01-APR-1999; 99US-0127462P.					
PR	06-APR-1999; 99US-0128234P.					
PR	08-APR-1999; 99US-0128714P.					
PR	16-APR-1999; 99US-0129845P.					
PR	19-APR-1999; 99US-0130077P.					
PR	21-APR-1999; 99US-0130449P.					

AAC47100
ID AAC47100 standard; DNA; 1095 BP.
XX
AC AAC47100;
XX
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52566.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
XX
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0030439.
XX
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
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PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161992P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
PR	04-AUG-1999;	99US-0147302P.			
PR	05-AUG-1999;	99US-0147192P.			
PR	05-AUG-1999;	99US-0147260P.			
PR	06-AUG-1999;	99US-0147303P.			
PR	06-AUG-1999;	99US-0147416P.			
PR	09-AUG-1999;	99US-0147493P.			
PR	09-AUG-1999;	99US-0147935P.			
PR	10-AUG-1999;	99US-0148171P.			
PR	11-AUG-1999;	99US-0148319P.			
PR	12-AUG-1999;	99US-0148341P.			
PR	13-AUG-1999;	99US-0148565P.			
PR	13-AUG-1999;	99US-0148684P.			
PR	16-AUG-1999;	99US-0149368P.			
PR	17-AUG-1999;	99US-0149175P.			
PR	18-AUG-1999;	99US-0149426P.			
PR	20-AUG-1999;	99US-0149722P.			
PR	20-AUG-1999;	99US-0149723P.			
PR	20-AUG-1999;	99US-0149929P.			
PR	23-AUG-1999;	99US-0149902P.			
PR	23-AUG-1999;	99US-0149930P.			
PR	25-AUG-1999;	99US-0150566P.			
PR	26-AUG-1999;	99US-0150884P.			
PR	27-AUG-1999;	99US-0151065P.			
PR	27-AUG-1999;	99US-0151066P.			
PR	27-AUG-1999;	99US-0151080P.			
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PR	30-AUG-1999;	99US-0151303P.	PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.	PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.	PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.	PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.	PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.	PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.	PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.	PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.	PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.	PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.	PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.	PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.	PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.	PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.	PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157553P.	PR	05-OCT-1999;	99US-0157553P.
PR	06-OCT-1999;	99US-0157865P.	PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.	PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.	PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.	PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.	PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.	PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.	PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159330P.	PR	14-OCT-1999;	99US-0159330P.
PR	14-OCT-1999;	99US-0159331P.	PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.	PR	14-OCT-1999;	99US-0159637P.
PR	14-OCT-1999;	99US-0159638P.	PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.	PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.	PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.	PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.	PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.	PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.	PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.	PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.	PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.	PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.	PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.	PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.	PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.	PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.	PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.	PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.	PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.	PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.	PR	29-OCT-1999;	99US-0162142P.
<hr/>					
Query Match 13.9%; Score 166.6; DB 3; Length 696;					
Best Local Similarity 59.0%; Pred. No. 1.3e-28;					
Matches 324; Conservative 0; Mismatches 219; Indels 6; Gaps 2;					
QY	439	TAGGAATGATGGTTCTCGAAAAGTACTGTGGGAAAGATTATGTCTGAAGTCTTGGTT	498		
DB	104	TAGGTATGATGGTTCCGGGAAACGACTGTAGGGAAGATTATGCGAAGATCGTGTGTT	163		
QY	499	ATTGCTTCTTTGATAGTGACCAAGTTAGTGGAGCAAGCTGTTGGAATGCCATCAGTTGCC	558		
DB	164	ATACATTTCTTTGATTGTGACACTTTGATCGAGCAGGCTATGAGGGAACCTCTGTAGCTG	223		
QY	559	AAATATTCAAGTCCATAGTAGGAAGCTTTCTTTGGGATAATGAGAGTAGTGTCTTTGAGAG	618		
DB	224	AGATATTGAGCATTTCCGTCGAGAGTGCTTTCAGAGAAAAGAGACTGAAGCGTTAAAGA	283		
QY	619	ATTGTCCTCCATG---CGACGATTAGTTGTGGCCACGGAGGTGGTGTGTATCCGAC	675		
DB	284	AACCTCTTTGATGTACCACCAAGTTGTTTTCACCGGGGGAGCGGCGAGTTATAAGAC	343		
QY	676	CAATTAACCTGGAGATATAGAGGGGCCCTATCTGTTTGGTTAGATGTGCCCTTGGATG	735		
DB	344	CCATCAATTGGAAGTACATGATTAAGGTATTAGTATTGGTTGATGTACCTCTAGAAG	403		

XX WPI; 2002-106200/14.
DR P-PSDB; ABP35328.
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and disorders related to organ
PT transplantation.
XX
XX Claim 1; Page 2393; 2508pp; English.
XX
XX Sequences ABP31028-ABP35561 represent 4534 novel human proteins
CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
CC ABN75987 represent cDNAs encoding them. The invention also encompasses
CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CC polynucleotides, the recombinant production of ORFX proteins, antibodies
CC specific for ORFX proteins, methods for detecting ORFX polynucleotides and
CC polypeptides, methods of screening for modulators of ORFX expression or
CC activity, and methods of screening individuals for a predisposition to an
CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC range of biological activities, such as cytokine, cell proliferation,
CC cell differentiation, immune modulation, haematopoiesis regulation,
CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic activity, thrombolytic activity,
CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
CC and antiinfective activity, and may also be involved in the determination
CC of bodily characteristics, fertility and behaviour. ORFX proteins,
CC nucleic acids and antibodies may be used in the treatment of cancers,
CC other proliferative disorders such as psoriasis and benign tumours,
CC neurological disorders such as epilepsy and Alzheimer's disease,
CC cardiovascular diseases, immune system disorders, disorders related to
CC organ transplantation, disorders of tissue growth and regeneration,
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
CC storage disease, and infectious diseases caused by viral, bacterial,
CC fungal and other pathogens. ORFX nucleic acids may also be used as a
CC source of primers and probes, in the detection of ORFX genomic sequences
CC or transcripts, in the identification and cloning of homologous
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC nucleic acids may additionally be used to produce transgenic animals
CC which may be useful for studying the function and/or activity of ORFX
CC protein, and in drug screening. The ORFX proteins may also be used as
CC immunogens to generate specific antibodies, which are useful in the
CC diagnosis, treatment and monitoring of ORFX-associated diseases
XX
XX Sequence 309 BP; 91 A; 65 C; 68 G; 85 T; 0 U; 0 Other;
SQ

Query Match 13.1%; Score 157; DB 6; Length 309;
Best Local Similarity 69.3%; Pred. No. 1.8e-26;
Matches 214; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 681 AACTGGAGATATATGAAGAGGGCCCTATCTGTTGGTTAGATGTCCTTGGATGCTTT 740
|||||
1 AATTTGGAGTTTACATGAAGAAAGCGCTGACCGTATGTTAGATGTCCTTGGATGCTTT 60
|||||

QY 741 GCTAGCGGTATTCCTAAAGTGGAACTGCTCTCTGCTCTTTCGACCAACCATCTGTT 800
|||||

DB 61 GCAAGAAGAAATTCCTGCTGTAGGAACCGCGTCTCGACCACTCTTTGATCAGGAATCCGGT 120
|||||

QY 801 GATCCGTACGCAATGGCCTTTTCTTAAGCTCAGCATGCTTCGACAGCAAGGGGTGATGCT 860
|||||

DB 121 GATCCTTATGCAAGGCTTATGCAAACTTACCTCACTTTTTCGACCAAGATGAGTCTG 180
|||||

QY 861 TATGCAAAATGCAGATGAAGGGTTTCTCTGGAAGAGATTGCAATGTAACAAGTCAATGAT 920
|||||

DB 181 TATGCTAATGCTGATGCGCAGAGTTTCACATTGAACATATGCAATTAACAAGGCCATAAT 240
|||||

QY 921 GATGTCCTTAAGCTGACCTACTGATATGCAATTTGCAATGAGTCACTTCAATAGATCGAGAC 980
|||||

DB 241 GATGTCACATATACCTTACACCTAGTACCATCGCCATTTGGGCATTTGTAAGATGGGAAT 300
|||||

QY 981 TTCGTATC 989

DB 301 TTCTTACC 309
|||
|||

RESULT 12
ADK58255
ID ADK58255 standard; DNA; 329 BP.
XX
XX AC ADK58255;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Plant DNA sequence which confers altered metabolic characteristic #5638.
XX
XX KW altered metabolic characteristic; plant; acid metabolism;
KW alcohol metabolism; fatty acid metabolism;
KW branched fatty acid metabolism; alkaloid metabolism;
KW amino acid metabolism; ester metabolism; glyceride metabolism;
KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;
KW terpene metabolism; isoprenoid metabolism; alkene metabolism;
KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX
XX OS Unidentified.
XX
XX PN WO2003020936-A1.
XX
XX PD 13-MAR-2003.
XX
XX PF 30-AUG-2002; 2002WO-US027884.
XX
XX PR 31-AUG-2001; 2001US-0316471P.
XX
XX PA (DOWC) DOW CHEM CO.
XX
XX PA (DOWC) DOW AGROSCIENCES LLC.
XX
XX PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX
XX WPI; 2003-313091/30.
XX
XX PT Novel genes that confer altered metabolic characteristics in Nicotiana
PT benthamiana plants, useful for altering the levels of metabolites e.g.
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX
XX PS Claim 1; SEQ ID NO 5638; 2576pp; English.
XX
XX CC The invention comprises DNA sequences which confer an altered metabolic
CC characteristic when they are expressed in a plant. The DNA sequences of
CC the invention are useful for producing plants with an altered metabolic
CC characteristic, such as: altered acid metabolism, alcohol metabolism,
CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
CC base metabolism, altered amino acid metabolism, altered ester metabolism,
CC altered glyceride metabolism, altered phenolic metabolism, altered
CC carbohydrate metabolism, altered sterol, oxygenated terpene, or
CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC metabolism, ketone or quinone metabolism. The DNA sequences of the
CC invention may be used to provide disease resistance in a plant and gene
CC shuffling or sexual PCR procedures. The present nucleic acid represents a
CC DNA sequence of the invention.
XX
XX SQ Sequence 329 BP; 93 A; 52 C; 88 G; 96 T; 0 U; 0 Other;

Query Match 11.5%; Score 138.4; DB 10; Length 329;
Best Local Similarity 64.9%; Pred. No. 3.7e-22;
Matches 205; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 412 ACTTGAACGGGAGGTGTTATTACCTAGTAGGATGATGGTTCCTGAAAGTACTGTG 471
|||||

DB 14 ATTTGAATGGAGATCTATGTACCTTGTGGATGATGGTTCCTGAAACACTGTG 73
|||||

QY 472 GGAAGATTATGTCTGAAGTCTTTGGGTATTTCGTTCTTTTATAGTAGTACAAAGTGTAGTGGAGC 531
|||||

Db 74 GRAAGTTAATGTCCAAAGTGCTGGTTATACGTTCTTTGACTGCGACACTTTGATTGAAC 133
Qy 532 AGCTGTTGAATGCATCAGTTGCGCCAAATATTCAAGTCCATAGTGAAGCTTCTTTC 591
Db 134 AGCGCATGAATGGAACCTCTGTTGTCAGAGATATTTGTTTCATCAGGAGAGAAATTTTTTA 193
Qy 592 GGGATAATGAGAGTAGTGTCTTGAGAGATTGTCCTCCATGCGACGATTAGTTGTTGCCA 651
Db 194 GAGGAAGAGACCGATGCGCTTAAGAAGCTCTCTTGAGGATATCAAGTTGTGTTTCCA 253
Qy 652 CCGAGGTGTTGTTATCCGACCAATTAACATGGAGATATATGAAGAGGGGCTATCTG 711
Db 254 CAGGTGAGGTGCAGTTATAAGACCCATTAACTGGAAGTATATGCAATGAAGGAATCAGCA 313
Qy 712 TTTGGTTAGATGTGCC 727
Db 314 TTTGGCTAGATGTGCC 329

RESULT 13

ACN52580/c

ID ACN52580 standard; cDNA; 573 BP.

XX

ACN52580;

XX

02-DEC-2004 (first entry)

XX

Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-N6-D8, SEQ:7361.

XX

Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium;
variety Nuoton33B; library LIB3828; molecular tag; molecular marker;
genetic mapping; molecular mapping; seed germination; plant growth;
plant quality; plant yield; plant breeding; tissue printing; ss.

XX

Gossypium hirsutum.

OS

US2004123340-A1.

XX

24-JUN-2004.

XX

12-DEC-2001; 2001US-00021323.

XX

14-DEC-2000; 2000US-0255619P.

XX

(DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

XX

Deikman J, Feng PCC, Fincher KL, Ziegler TE;

PI

WPI; 2004-479808/45.

XX

New isolated nucleic acid molecule that encodes a plant protein or its
fragment, useful for isolating a variety of agronomically significant
genes associated with plant growth, quality or yield, and as molecular
tags to map genes.

XX

Claim 1; SEQ ID NO 7361; 34pp; English.

PS

The invention relates to 17880 cotton expressed sequence tags (ESTs;
ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
from primed or non-primed seeds from variety DP50B, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoeium
tissue, developing fibres, carpal walls and septa from variety
Nuoton33B. The invention also relates to substantially purified
proteins or their fragments encoded by nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid construct
comprising a nucleic acid of the invention. The cotton ESTs are useful as
molecular tags to isolate genetic regions, to isolate genes, to map
genes, to determine gene function and to determine whether genes are
members of a particular gene family. The nucleic acid molecules may be
used for isolating a variety of agronomically significant genes

CC

CC associated with plant growth, quality, yield, and could also serve as
links in metabolic and catabolic pathways. The nucleic acid molecules are
also useful for identifying genes important in initiating and maintaining
seed germination or that may be used to mitigate stresses encountered
during seed germination. The ESTs additionally enable the acquisition of
promoters and cis-regulatory elements which will be useful to express
agronomically significant genes in these tissues and/or other tissues,
and also permits the acquisition of molecular markers useful in breeding
schemes, genetic and molecular mapping, and in cloning of agronomically
significant genes. The nucleic acid molecules are further useful for
detecting the expression level or pattern of a protein or mRNA and for
detecting the presence or quantity of a protein by tissue printing. The
present sequence represents a specifically claimed EST isolated from a
cotton variety Nuoton33B androecium tissue cDNA library (LIB3828). The
sequence data for this patent did not form part of the printed from the US
specification, but was obtained in electronic format directly from the US
patent office at seqdata.uspto.gov/sequence.html?docID=US20040123340
XX

SQ Sequence 573 BP; 183 A; 138 C; 86 G; 166 T; 0 U; 0 Other;

Query Match 11.3%; Score 135.2; DB 13; Length 573;

Best Local Similarity 64.4%; Pred. No. 2.4e-21;

Matches 219; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

Qy 628 CCATGCGACGATTAGTTGTCACCGGAGGTGGTCTTATCCGACCAATTAACCTGA 687

Db 573 CAAAGAAACAACCTGTTGTTCTACTGTGGAGGTGCAGTTGTACTGTGACTGCGG 514

Qy 688 GATATAT---GAAGAGGGGCTTATCTGTTGGTTAGATGTCCTTGGATGCTCTTGCTA 744

Db 513 ACTATATGCAGAGAAGGGGATGTTGTTGGTTAGATGTACTTTGGAAGCTTTGGCAC 454

Qy 745 GCGTATTGCTAAAGTGGGAACCTGCTCTGCTCTTCTGACCAACCATCTGCTGATC 804

Db 453 AAAGGATTGCTGCAGTAGTACTTCTCTGCTCCCTTTGTCATTATGAAGATGGTGATC 394

Qy 805 CGTACGCAATGCGCTTTTCTAAGCTCAGCATCTTTCGACAGCAAGGGGTGATGCTTATG 864

Db 393 CATATACAAGGCTTTAAACGTCCTTACCTTTTGGAGCAGAGGGGTAATAATATG 334

Qy 865 CAAATGCAGATGTAAGGGTTTCTCTGGAAGAGATTGCATGTAAACAAGGTCAATGATG 924

Db 333 CTAAAGCAAATGCCAGGGTTTCATTGTAAAGAAATTCCTGGCAAACTAGGTTATAGATG 274

Qy 925 TCTCTAAGCTGACACCTACTGATATGCAATTTGAGTCACT 964

Db 273 TATCAGATCTTACTCCACAGAGATCGCAATCGAGGCATT 234

RESULT 14

ADR60835

ID ADR60835 standard; cDNA; 1010 BP.

XX

ADR60835;

AC

02-DEC-2004 (first entry)

XX

Cotton cDNA sequence, SEQ ID 1616.

XX

Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
drought tolerance; plant disease resistance; galactomannan; lignin;
plant growth regulator; heat tolerance; herbicide tolerance;
homologous recombination; extreme osmotic condition tolerance;
pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
stress resistance.

XX

Gossypium hirsutum.

OS

US2004181830-A1.

XX

16-SEP-2004.

XX

29-JAN-2004; 2004US-00767795.

XX

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2005, 16:54:33 ; Search time 367 Seconds
(without alignments)
5350.224 Million cell updates/sec

Title: US-10-660-226-9
Perfect score: 1200
Sequence: 1 cgcgcaccagctaccctgcc.....aaaaaaaaaaaaaaaaaaaa 1200

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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3: /cgn2_6/prodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/1/ina/PCUS_COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	4.6	603	US-09-328-352-2023	Sequence 2023, Ap
2	53.8	4.5	1733	US-09-073-569-1	Sequence 1, Appli
3	53	4.4	1154	US-08-651-136C-7	Sequence 7, Appli
4	53	4.4	1154	US-09-229-911A-7	Sequence 7, Appli
5	52.8	4.4	222	US-08-481-190-15	Sequence 15, Appl
6	52.8	4.4	222	PCT-US93-00869-15	Sequence 15, Appl
7	52.6	4.4	1308	US-10-151-832-1	Sequence 1, Appli
8	52.6	4.4	1447	US-09-443-041A-27	Sequence 27, Appl
9	52.6	4.4	2045	US-09-152-060-22	Sequence 22, Appl
10	52.6	4.4	3871	US-08-599-455B-3	Sequence 3, Appli
11	52.6	4.4	3871	US-09-069-781B-3	Sequence 3, Appli
12	52.6	4.4	3871	US-09-137-132-3	Sequence 3, Appli
13	52.6	4.4	3871	US-08-864-564A-3	Sequence 3, Appli
14	52.6	4.4	3871	US-09-094-410-3	Sequence 3, Appli
15	52.6	4.4	3871	US-08-708-123D-3	Sequence 3, Appli
16	52.6	4.4	3871	US-08-583-153A-3	Sequence 3, Appli
17	52.6	4.4	3871	US-08-570-142D-3	Sequence 3, Appli
18	52.6	4.4	3871	US-08-638-524B-3	Sequence 3, Appli
19	52.4	4.4	1509	US-09-149-476-179	Sequence 179, App
20	52.2	4.4	2187	US-09-127-219B-2	Sequence 2, Appli
21	52.2	4.4	2267	US-09-917-265A-107	Sequence 107, App
22	52.2	4.4	2267	US-09-917-265A-109	Sequence 109, App
23	52	4.3	153	US-09-621-976-18058	Sequence 18058, A
24	52	4.3	160	US-09-621-976-18071	Sequence 18071, A
25	52	4.3	162	US-09-621-976-18068	Sequence 18068, A
26	52	4.3	179	US-09-621-976-18054	Sequence 18054, A
27	52	4.3	396	US-09-640-173-10	Sequence 10, Appl

c	28	52	4.3	396	4	US-09-713-550-10	Sequence 10, Appl
c	29	52	4.3	396	4	US-09-825-294-10	Sequence 10, Appl
c	30	52	4.3	396	4	US-09-970-966-10	Sequence 10, Appl
	31	51.8	4.3	1100	3	US-07-861-458C-4	Sequence 4, Appli
	32	51.6	4.3	1225	1	US-08-286-020-1	Sequence 1, Appli
	33	51.6	4.3	1225	1	US-08-603-919-1	Sequence 1, Appli
	34	51.6	4.3	1530	4	US-09-811-361-19	Sequence 19, Appl
	35	51.4	4.3	1512	2	US-08-909-965C-8	Sequence 8, Appli
	36	51.4	4.3	1602	3	US-09-402-929-1	Sequence 1, Appli
	37	51.2	4.3	160	4	US-09-621-976-18066	Sequence 18066, A
	38	51.2	4.3	1297	4	US-09-800-729-80	Sequence 80, Appl
c	39	51.2	4.3	3138	1	US-07-867-106-4	Sequence 4, Appli
	40	50.8	4.2	351	4	US-09-621-976-15134	Sequence 15134, A
	41	50.8	4.2	976	2	US-08-504-459-9	Sequence 9, Appli
	42	50.8	4.2	2080	4	US-10-003-392-1	Sequence 1, Appli
	43	50.8	4.2	6065	4	US-09-800-729-35	Sequence 35, Appl
	44	50.8	4.2	28257	4	US-09-949-016-13076	Sequence 13076, A
	45	50.6	4.2	1414	4	US-09-501-115-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-328-352-2023
; Sequence 2023, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2023
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2023

Query Match 4.6%; Score 55; DB 4; Length 603;
Best Local Similarity 52.8%; Pred. No. 0.00012;
Matches 143; Conservative 0; Mismatches 125; Indels 3; Gaps 1;

QY	428	TATTTACCTAGTACGAATGATGGTTCTGGAAGAAAGTACTGTGGGAAGATTATGCTGA	487
Db	93	TATTTATTTGGTAGGCCCATGGGGCAGGAAACAAACCGTTGGACGTCATTTAGCAGA	152
QY	488	AGTCTTGGGTTATTTCGTTCTTTGTATGACAAAGTTAGTGAGCAAGCTGTTGGAATGCC	547
Db	153	ACTATTAGGGCGTGAATTTTATAGATAGTATGATGAATTTGAGCGCAAGACAGG---	209
QY	548	ATCAGTTGCCCAATATTCAGAGTCCATAGTGAAGCCCTTTTCGGGATATGAGAGTAG	607
Db	210	CACATATTCCTGGATTTTGAAGAAAGAGAGAGTCCGCTTCCGTCGCGTGAACCTGT	269
QY	608	TGCTTTGAGAGATTGTCCTCATCGCAGCATTTGTTGCCACCGGAGGTGGTCTGT	667
Db	270	CGTTTTAAATGAGCTTACTTCACGTAAGCATTTAGTGTTCGCCAGGTGGCGTGCTAT	329
QY	668	TATCGACCAATTAAGTGGAGATATATGAAG	698
Db	330	TACTCAGGCGCTAATCGGGAGTTTTTAAAG	360

RESULT 2
US-09-073-569-1
; Sequence 1, Application US/09073569
; Patent No. 6084088
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Grosseman, Angelika


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;
; FILING DATE: 13-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/651,136
; FILING DATE: 21-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4366.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..935
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-229-911A-7

Query Match 4.4%; Score 53; DB 3; Length 1154;
Best Local Similarity 65.8%; Pred. No. 0.00059;
Matches 77; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1084 ACATAGAGCATCTTGAGTTATTGTTAAAGGAATGGAAGGAGGAGCTAATATCCGAAG 1143
Db 1025 ATATAGTCTTCCGAGTACATACATTGTAATGAAATGAAGCGGCTCGGACCATGAGCAG 1084

QY 1144 TGTGCGCTTGGCTGAAAAA 1200
Db 1085 ATGCCATTGATAAAAAA 1141

RESULT 5
US-08-481-190-15
; Sequence 15, Application US/08481190
; Patent No. 6160204
; GENERAL INFORMATION:
; APPLICANT: John C. Steffens
; TITLE OF INVENTION: Polyphenol Oxidase cDNA
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,190
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION:
; APPLICATION NUMBER: 203,533
; FILING DATE: 02-24-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: UA 816 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 15:
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-481-190-15

Query Match 4.4%; Score 52.8; DB 3; Length 222;
Best Local Similarity 71.9%; Pred. No. 0.00028;
Matches 69; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1105 TTTGTAAGGAATGGAAGGAGGAGCTAATATCCGAAGTGTGCCGTGCGCTGAAAAA 1164
Db 122 TTGTTAATGCTATGTATGAAATAAATAAATGTTCTTCCATTTAATTTTAAAAA 181

QY 1165 AAAAAA 1200
Db 182 AAAAAA 217

RESULT 6
PCT-US93-00869-15
; Sequence 15, Application PC/TUS9300869
; GENERAL INFORMATION:
; APPLICANT: John C. Steffens
; TITLE OF INVENTION: Polyphenol Oxidase cDNAs: Cloning
; TITLE OF INVENTION: and Applications
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00869
; FILING DATE: 19930129
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: CRF D-1057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US93-00869-15

Query Match 4.4%; Score 52.8; DB 5; Length 222;
Best Local Similarity 71.9%; Pred. No. 0.00028;
Matches 69; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1105 TTTGTAAGGAATGGAAGGAGGAGCTAATATCCGAAGTGTGCCGTGCGCTGAAAAA 1164
Db 122 TTGTTAATGCTATGTATGAAATAAATAAATGTTCTTCCATTTAATTTTAAAAA 181

QY 1165 AAAAAA 1200
Db 182 AAAAAA 217
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STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3871 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 194...3688
US-08-599-455B-3

Query Match 4.4%; Score 52.6; DB 2; Length 3871;
Best Local Similarity 66.1%; Pred. No. 0.0014;
Matches 76; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1086 ATAGAGCATCGTTGAGTTATTTGTAAGGAATCGAAGAGGAGCTAATAATCCGAGTG 1145
DB 3744 ATAGATTATAGTTGTGGTGGGAGAGAGAAAGAAACCGAGTCCAAATTTGAAAAATAAT 3803

QY 1146 TGCCGTTGGCTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1200
DB 3804 TGTTCCCACTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 3858

RESULT 11
US-09-069-781B-3
Sequence 3, Application US/09069781B
Patent No. 6287782
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
```

```
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,781B
FILING DATE: 29-APRIL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3871 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 194...3688
US-09-069-781B-3

Query Match 4.4%; Score 52.6; DB 3; Length 3871;
Best Local Similarity 66.1%; Pred. No. 0.0014;
Matches 76; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1086 ATAGAGCATCGTTGAGTTATTTGTAAGGAATCGAAGAGGAGCTAATAATCCGAGTG 1145
DB 3744 ATAGATTATAGTTGTGGTGGGAGAGAGAAAGAAACCGAGTCCAAATTTGAAAAATAAT 3803

QY 1146 TGCCGTTGGCTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1200
DB 3804 TGTTCCCACTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 3858

RESULT 12
US-09-137-132-3
Sequence 3, Application US/09137132
Patent No. 6380363
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
```

;; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
;; NUMBER OF SEQUENCES: 50
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson, P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; FILING DATE: 18-AUG-1998
;; PRIORITY APPLICATION DATA:
;; FILING DATE: 28-MAY-1997
;; APPLICATION NUMBER: 08/864,564
;; FILING DATE: 28-MAY-1997
;; APPLICATION NUMBER: 08/708,123
;; FILING DATE: 03-SEP-1996
;; APPLICATION NUMBER: 08/638,524
;; FILING DATE: 26-APR-1996
;; APPLICATION NUMBER: 08/599,455
;; FILING DATE: 22-JAN-1996
;; APPLICATION NUMBER: 08/583,153
;; FILING DATE: 28-DEC-1995
;; APPLICATION NUMBER: 08/570,142
;; FILING DATE: 11-DEC-1995
;; APPLICATION NUMBER: 08/569,485
;; FILING DATE: 08-DEC-1995
;; APPLICATION NUMBER: 08/566,622
;; FILING DATE: 04-DEC-1995
;; APPLICATION NUMBER: 08/562,663
;; FILING DATE: 27-NOV-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meiklejohn, Ph.D., Anita L.
;; REGISTRATION NUMBER: 35,283
;; REFERENCE/DOCKET NUMBER: 07334/019004
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3871 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: unknown
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: Coding Sequence
;; LOCATION: 194...3688
US-09-137-132-3

Query Match 4.4%; Score 52.6; DB 3; Length 3871;
Best Local Similarity 66.1%; Pred. No. 0.0014;
Matches 76; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1086 ATAGAGCATCGTTGAGTTATTTGTAAGGAAGGAGGAGCTAATAATCCGAAGTG 1145
Db 3744 ATAGATTATAGTTGTGGTGGGAGAGAGAAACCCAGAGTCCAAAATTTGAAAATAAT 3803
QY 1146 TCCCGTTGGCTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1200
Db 3804 TGTTCCTCAACTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 3858

RESULT 13
US-08-864-564A-3
; Sequence 3, Application US/08864564A
; Patent No. 6395498

;; GENERAL INFORMATION:
;; APPLICANT: Tartaglia, Louis A.
;; APPLICANT: Tepper, Robert I.
;; APPLICANT: Culpepper, Janice A.
;; APPLICANT: White, David W.
;; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
;; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
;; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
;; NUMBER OF SEQUENCES: 50
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson, P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; FILING DATE: 28-MAY-1997
;; APPLICATION NUMBER: US/08/864,564A
;; PRIORITY APPLICATION DATA:
;; FILING DATE: 03-SEP-1996
;; APPLICATION NUMBER: 08/708,123
;; FILING DATE: 26-APR-1996
;; APPLICATION NUMBER: 08/638,524
;; FILING DATE: 22-JAN-1996
;; APPLICATION NUMBER: 08/599,455
;; FILING DATE: 28-DEC-1995
;; APPLICATION NUMBER: 08/583,153
;; FILING DATE: 11-DEC-1995
;; APPLICATION NUMBER: 08/570,142
;; FILING DATE: 08-DEC-1995
;; APPLICATION NUMBER: 08/569,485
;; FILING DATE: 04-DEC-1995
;; APPLICATION NUMBER: 08/566,622
;; FILING DATE: 27-NOV-1995
;; APPLICATION NUMBER: 08/562,663
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meiklejohn, Ph.D., Anita L.
;; REGISTRATION NUMBER: 35,283
;; REFERENCE/DOCKET NUMBER: 07334/019002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3871 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: unknown
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: Coding Sequence
;; LOCATION: 194...3688
US-08-864-564A-3

Query Match 4.4%; Score 52.6; DB 3; Length 3871;
Best Local Similarity 66.1%; Pred. No. 0.0014;
Matches 76; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1086 ATAGAGCATCGTTGAGTTATTTGTAAGGAAGGAGGAGCTAATAATCCGAAGTG 1145
Db 3744 ATAGATTATAGTTGTGGTGGGAGAGAGAAACCCAGAGTCCAAAATTTGAAAATAAT 3803
QY 1146 TCCCGTTGGCTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1200
Db 3804 TGTTCCTCAACTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 3858

RESULT 14
US-09-094-410-3
; Sequence 3, Application US/09094410
; Patent No. 6403552
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,410
; FILING DATE: 09-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
US-09-094-410-3

Query Match 4.4%; Score 52.6; DB 3; Length 3871;
Best Local Similarity 66.1%; Pred. No. 0.0014;
Matches 76; Conservative 39; Indels 0; Gaps 0;
QY 1086 ATAGACATCGTTGAGTATTATTTTAAAGGAATGGAAGAGGAGCTTAATAATCCGAAGTG 1145

Db 3744 ATAGATTATAGTTGTGGGTGGAGAGAGAAAGAACCCAGAGTCCAAATTTTGAATAAT 3803
QY 1146 TGCCCGTGTGCTGAAA 1200
Db 3804 TGTCCCACTGAAA 3858
RESULT 15
US-08-708-123D-3
; Sequence 3, Application US/08708123D
; Patent No. 6482927
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/708,123D
; FILING DATE: 03-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 194...3688
US-08-708-123D-3
Query Match 4.4%; Score 52.6; DB 4; Length 3871;
Best Local Similarity 66.1%; Pred. No. 0.0014;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2005, 17:26:08 ; Search time 888 Seconds
(without alignments)
8842.013 Million cell updates/sec

Title: US-10-660-226-9
Perfect score: 1200
Sequence: 1 cgcgcaccagctacctgccc.....aaaaaaaaaaaaaaaaaaaa 1200

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7331713 seqs, 3271544945 residues

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	1200	18	US-10-660-226-9
2	1045.4	87.1	1059	18	US-10-425-114-30672
3	988.2	82.3	1474	20	US-10-425-115-16472
4	846.2	70.5	1228	18	US-10-425-114-35273
5	843.4	70.3	1593	20	US-10-425-115-16474
6	841.8	70.2	1241	18	US-10-425-114-31574
7	805	67.1	1273	19	US-10-767-701-13420

8	737.4	61.4	838	20	US-10-425-115-16473
9	660	55.0	1410	19	US-10-437-963-45320
10	574	47.8	1061	18	US-10-660-226-27
11	370	30.8	1223	20	US-10-739-930-4532
12	367.8	30.6	1503	20	US-10-425-115-68871
13	364.4	30.4	1523	18	US-10-660-226-25
14	363.4	30.3	999	18	US-10-660-226-11
15	362.6	30.2	960	18	US-10-660-226-19
16	352.6	29.4	738	20	US-10-425-115-16469
17	352.4	29.4	657	18	US-10-424-599-62654
18	342.2	28.5	1147	19	US-10-437-963-84942
19	335.2	27.9	536	18	US-10-425-114-6610
20	323.8	27.0	641	20	US-10-739-930-1680
21	293	24.4	397	19	US-10-437-963-84944
22	270	22.5	544	18	US-10-660-226-15
23	241.6	20.1	1327	18	US-10-425-114-29872
24	241.6	20.1	1354	18	US-10-424-599-70058
25	233.6	19.5	637	21	US-10-487-901-57
26	231.2	19.3	492	18	US-10-424-599-25738
27	227	18.9	1041	19	US-10-767-701-11266
28	222.6	18.6	1256	19	US-10-437-963-2340
29	206.2	17.2	365	20	US-10-425-115-151552
30	193.2	16.1	488	20	US-10-425-115-162636
31	193	16.1	1332	20	US-10-739-930-523
32	191	15.9	967	18	US-10-424-599-137299
33	191	15.9	967	18	US-10-425-114-29612
34	190.4	15.9	524	18	US-10-425-114-18884
35	163	13.6	660	21	US-10-487-901-5640
36	162.2	13.5	407	20	US-10-425-115-158029
37	157	13.1	309	11	US-09-864-408A-8601
38	149.8	12.5	696	19	US-10-437-963-2317
39	149.2	12.4	676	20	US-10-425-115-145002
40	141.4	11.8	1096	18	US-10-424-599-11365
41	139.4	11.6	1183	18	US-10-660-226-21
42	138.4	11.5	329	21	US-10-487-901-5638
43	137.4	11.5	513	18	US-10-424-599-19179
44	135.2	11.3	573	19	US-10-021-323-7361
45	131.2	10.9	332	20	US-10-425-115-33448

ALIGNMENTS

RESULT 1

US-10-660-226-9
; Sequence 9, Application US/10660226
; Publication No. US20040064848A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Rendina, Alan
; TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
; FILE REFERENCE: BB-1159-C
; CURRENT APPLICATION NUMBER: US/10/660,226
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/09/354,501
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1200
; TYPE: DNA
; ORGANISM: Zea mays
US-10-660-226-9

Query Match 100.0%; Score 1200; DB 18; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 AGTGTGCTGTTATCCGACCAATTAACCTGGAGATATATGAAGAGGGGCTATCTGTTTG 715
Db 541 AGTGTGCTGTTATCCGACCAATTAACCTGGAGATATATGAAGAGGGGCTATCTGTTTG 600
QY 716 GTTAGATGTCCTCGCTGCTGCTAGGCGTATTGCTAAAGTGGAACTGCCTCTCG 775
Db 601 GTTAGATGTCCTCGCTGCTGCTAGGCGTATTGCTAAAGTGGAACTGCCTCTCG 660
QY 776 TCTCTTCTGGACCAACCAATCTGGTATCCGTACGCAATGGCCCTTTTCTAAGCTCAGCAT 835
Db 661 TCTCTTCTGGACCAACCAATCTGGTATCCGTACGCAATGGCCCTTTTCTAAGCTCAGCAT 720
QY 836 GCTTGACACAAAGGGGTGATGCTTATGCAAAATCAGATGTAAGGGTTTCTCTGGAAGA 895
Db 721 GCTTGACACAAAGGGGTGATGCTTATGCAAAATCAGATGTAAGGGTTTCTCTGGAAGA 780
QY 896 GATTGATCTTAACRAGGTCTGATGATGCTCTTAAGCTGACACCTACTGATATTGCAAT 955
Db 781 GATTGATCTTAACRAGGTCTGATGATGCTCTTAAGCTGACACCTACTGATATTGCAAT 840
QY 956 TGAGTCACTTCAATAGATCGAGAGCTTCGTATCGAGCACACTGCTGATAGTTCAGCTAG 1015
Db 841 TGAGTCACTTCAATAGATCGAGAGCTTCGTATCGAGCACACTGCTGATAGTTCAGCTAG 900
QY 1016 CGACGGCGAAGCTGAGTCCGAGATCCAGAGGATACAGACCTTTGTAAGCTTTAATCCCTT 1075
Db 901 CGACGGCGAAGCTGAGTCCGAGATCCAGAGGATACAGACCTTTGTAAGCTTTAATCCCTT 960
QY 1076 TGTGTTGCCACATAGACATCGTTGAGTTATTTGTAAAGAAATGGAAGAGGGAGCTTAATA 1135
Db 961 TGTGTTGCCACATAGACATCGTTGAGTTATTTGTAAAGAAATGGAAGAGGGAGCTTAATA 1020
QY 1136 ATCCGAAGTGTGCGCTTGCTGAAAAA 1162
Db 1021 ATCCGAAGTGTGCGCTTGCTGAAAAA 1047

RESULT 3

US-10-425-115-16472
; Sequence 16472, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 16472
; LENGTH: 1474
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_115020C.1
US-10-425-115-16472

Query Match 82.3%; Score 988.2; DB 20; Length 1474;
Best Local Similarity 93.8%; Pred. No. 4.9e-261;
Matches 1042; Conservative 0; Mismatches 63; Indels 6; Gaps 1;
QY 52 GGATCCTCAGAGATCAGAGATTCAGTTGAGCTATAGCGGTAGCCGATCGGTGCCGC 111
Db 4 GGACCTCGAGGCGCGCGGAGTCTGATCCGACTAGTCCGCGCGTCTCTTCCCGC 63
QY 112 GTCCCTCTCGGTCCACCGGCGGAGCAATGGAGGGGGCGTCCGCTGGCG 171
Db 64 GCAGCAGCAGAGCACACCGCGAGCGAGCAATGAGCGGGGGCGTGGCGC 123
QY 172 TGCAGGCGGGGGGGGCTTCGGCTCCAGCGGCGACCGGGCGGCGCTACAGGGGCCCA 231

RESULT 4

US-10-425-114-35273
; Sequence 35273, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:

Db 124 TCACAGACGGCGCGCGGCTTCGGCTCCGACAGCGCGCGGCGGCTTACAGTCGCCCA 183
QY 232 CGGAGAGCTGAGAGTCCGTGACCGCGGGGACCTGCGGTCCGTGCGGGCTCCGGGT 291
Db 184 TCGGAGAGCTGAGAGTCCGTGACCGCGGGGACCTGCGGTCCGTGCGGGTTCGGGT 243
QY 292 CCAAGCCGCTCCACACCGCTCCGACTCCGTCGCGAAGAAATCGTCCGAGAGTCATGAAAACT 351
Db 244 CCAAGCCGCTCCACACCGCTCCGACTCCGTCGCGAAGAAATCGTCCGAGAGTCATGAAAACT 297
QY 352 CGCAACAATCCCTTGAAGAGCTCCCTGTTGAAAGAAAAATCAGAAAGTTCGTGTTCT 411
Db 298 TGCATAAATCCCTTGAAGAGCACTCCCTGTTGAAAGAAAAATCAGAAAGTTCGTGTTCT 357
QY 412 ACTTCGAACGGGAGGTGTTTACCTAGTAGGAATCATGGGTCTCGAAAAAGTACTGTGG 471
Db 358 ACTTAAACCGGAGGTGTTTAACTTAGTGGGAATCATGGGTCTCGAAAAAGTACTGTGG 417
QY 472 GGAAGATTATGTCTGAAGTCTTTGGGTATTTCCGTTCTTTGATAGTGAAGAATTTAGTGAGC 531
Db 418 GGAAGATTATGTCTGAAGTCTTTGGGTATTTCCGTTCTTTGATAGTGAAGAATTTAGTGAGC 477
QY 532 AAGCTGTTGGAATGCAATCAGTTGCCAAATATTCAAGTCCATAGTGAAGCTTCTTTTC 591
Db 478 AAGCTGTTGGAATGCAATCAGTTGCCAAATATTCAAGTCCATAGTGAAGCTTCTTTTC 537
QY 592 GGGTAATGAGAGTATGCTTGAGAGATTTGCTCCATCGAGAGATTTAGTTGTTGCCA 651
Db 538 GGGTAATGAGAGTATGCTTGAGAGATTTGCTCCATCGAGAGATTTAGTTGTTGCCA 597
QY 652 CCGGAGTGGTCTGTTATTCGACCAATTAACCTGGAGATATATGAAGAGGGCCTATCTG 711
Db 598 CCGGAGTGGTCTGTTATTCGACCAATTAACCTGGAGATATATGAAGAGGGCCTATCTG 657
QY 712 TTTGTTAGATGTCCTTTGGATGCTCTTGTAGCGGTATTCCTAAAGTGGAACTGTCCT 771
Db 658 TTTGTTAGATGTCCTTTGGATGCTCTTGTAGCGGTATTCCTAAAGTGGAACTGTCCT 717
QY 772 CTCGTCCTTCTTGACCAACCATCTGCTGATCCGTACGCAATGGCCTTTCTTAAGCTCA 831
Db 718 CTCGTCCTTCTTGACCAACCATCTGCTGATCCGTACGCAATGGCCTTTCTTAAGCTCA 777
QY 832 GCATGCTTGACAGCAAAAGGGGTGATGCTTATGCAAAATGCAGATGTAAAGGGTTCTCTGG 891
Db 778 GCATGCTTGACAGCAAAAGGGGTGATGCTTATGCAAAATGCAGATGTAAAGGGTTCTCTGG 837
QY 892 AAGAGATTGCATGTAAAAAAGGTCAATGATGCTCTTAAGCTGACACCTACTGATATTG 951
Db 838 AAGAGATTGCATGTAAAAAAGGTCAATGATGCTCTTAAGCTGACACCTACTGATATTG 897
QY 952 CAAATTGAGTCACTTCATTAAGATCGAGAGCTTCGTATCGAGCACACTGCTGATAGTTAG 1011
Db 898 CAAATTGAGTCACTTCATTAAGATCGAGAGCTTCGTATCGAGCACACTGCTGATAGTTAG 957
QY 1012 CTAGCGACGCGCAAGCTGAGTCGAGATCCAGAGATACAGACCTTTGTAGAACTTAAATC 1071
Db 958 CTAGCGACGCGCAAGCTGAGTCGAGATCCAGAGATACAGACCTTTGTAGAACTTAAATC 1017
QY 1072 CTTTTGTTTGGCACAATAGAGCATCGTTGAGTTATTTGTAAGAAATGGAAGAGGAGCT 1131
Db 1018 CTTTTGTTTGGCACAATAGAGCATCGTTGAGTTATTTGTAAGAAATGGAAGAGGAGCT 1077
QY 1132 AATAATCCGAAGTGTGCGCTGAAAAA 1162
Db 1078 AATAATCCGAAGTGTGCGCTGAAAAA 1108

Db 331 AACCGCGGAGCTGCGGTTGCCGTCGGGTTCCGCGGTTCCAGCCCGTCGTACCG---- 386
Qy 313 GACTCCGTCGAAGAAATCCGTCGGAGGTCATGAAATCTCGCAAACTCCGTTGACGAAG 372
Db 387 --CTCCGTCGAAGAAATCATCCGAGGTCATGAAATCTGCAATCTCGTTGACGAAG 444
Qy 373 CTCCTCTGTTGAAGAGAAATCAGAAGAGTTCTGTTCTACTTTGAACGGGAGGTGATTT 432
Db 445 CTCCTCTGTTGAAGAGAAATCAGAAGAGTTCTGTTCTACTTTAAACGGGAGGTGATTT 504
Qy 433 ACCTAGTAGGAATGAGGTTCTGGAAAAGTACTGTGGGAAGATTAATGTCGAAGTCT 492
Db 505 ACTTAGTGGGAATGAGGTTCTGGAAAAGTACTGTGGGAAGATTAATGTCGAAGTCT 564
Qy 493 TGGGTTATTCGTTCTTTGATAGTACAAAGTTAGTGGGAAGAGTGTGGAATGCCATCAG 552
Db 565 TGGGTTATTCGTTCTTTGATAGTACAAATAGTGGGAAGAGTGTGGAATGCCATCAG 624
Qy 553 TTGCCAAATATTCAGAGTCCATAGTGAAGCCTTTCTTTGGGATTAATGAGAGTAGTGTCT 612
Db 625 TTGCTCAAAATATTCAGAGTCCATAGTGAAGCCTTTCTTTGGGATTAATGAGAGTAGTGTCT 684
Qy 613 TGAGAGATTGTCCTCCATCGGAGGATTAAGTGTGTCACCGAGGTCGTGCTGTTATCC 672
Db 685 TGAGGAGTGTCTCTCATCGGAGGATTAAGTGTGTCACCGAGGTCGTGCTGTTATCC 744
Qy 673 GACCAATTAAGTGGAGATTAATGAAGAGGCGCTATCTGTTGTTAGATGTGCCCTTGG 732
Db 745 GACCAGTTAACTGGAAATATGAAGAGGCGCTATCCGTTTGGTTAGATGTGCCCTTGG 804
Qy 733 ATGCTCTTGTAGCGGATTTGCTAAAGTGGGAATCGCTCTCGTCTCTTCTGGACCAAC 792
Db 805 ATGCTCTTGTAGCGGATTTGCTAAAGTGGGAATCGCTCTCGTCTCTTCTGGACCAAC 864
Qy 793 CATCTGGTGTGCTAGCGAATGGCCTTTCTTAAGCTCAGCATGCTTGACGCAAGGG 852
Db 865 CGTCCGGTGTGATCATACAAATGGCCTTTCTTAAGCTCAGCATGCTTGACGCAAGGG 924
Qy 853 GTGATGCTTATGCAAAATGCAAGTGTAAAGGTTTCTTGGGAAGATTTGATGTAAACAAG 912
Db 925 GTGATGCTTATGCAAAATGCGGATGTAAAGGTTTCTTGGGAAGATTTGATGTAAACAAG 984
Qy 913 GTCATGATGATGCTCTTAAGCTGACACCTACTGATATTCGATATTCGATGCTTCTCATAGA 972
Db 985 GTCATGCGATGCTCTAAGCTGATCGGACTGATATCGCAATGAGTCACTTCTCATAGA 1044
Qy 973 TCGAGAGCTTCGTCATCGAGCACCTGCTGATAGTTTCAAGTACGCGAGCGCAAGTGT 1032
Db 1045 TCGAGAGTTTCGTCATCGAGCACGCTGCTGATTAATCCAGCTAGCGACTCGCAAGCTGAGT 1104
Qy 1033 CGCAGATCCAGAGATACAGACCTTGTAGAACCTTAATCCCTTTGTTGCCAC 1085
Db 1105 CACAGATCCAAAGATACAGACCTTGTATATCTTAATCTCTGTTTGTATC 1157

RESULT 6
US-10-425-114-31574
; Sequence 31574, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ IDS: 73128
; SEQ ID NO 31574

; LENGTH: 1241
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73191D05_FLI
US-10-425-114-31574

Query Match 70.2%; Score 841.8; DB 18; Length 1241;
Best Local Similarity 87.9%; Pred. No. 8.8e-221;
Matches 943; Conservative 0; Mismatches 122; Indels 8; Gaps 2;

Qy 15 CTTGCTTCTCTCTCTCTTTTACCTCTCACTCCGATCGCTCAGAGTTCAG--AG 72
Db 30 CTTGCTTCTCTCTCTCTCTTTTCTAGACCCCGGATCGCTCAGAGTTCAGTCT 89
Qy 73 ATTCCAGTTGAGCTATAGCGGTAGCGACTGCTGCGCGGCTCCCTCTCGGCTCCACCCG 132
Db 90 AGTCGTATCCCGACTAGTCGCCGCTCTCTTTTCCCGCGCAGCAGCAGCACCACCCG 149
Qy 133 GCGAGCGAAATGAGGCGCGGGGCGTCGCGCTGCGCTGCGAGCGCGGGCGCGGGCT 192
Db 150 GTGACCGAGCAATGAGGCGCGGGGCGTGGGCTGCGCTGCGAGCGCGGGCGGGCT 209
Qy 193 TCGGCTTCCAGCCGCGCACCGGGCGGCTTACAGCGCGCCACCGGAGCTTGAAGTTCGCTG 252
Db 210 TCGGCTTCCAGCCGCGCACCGGGCGGCTTACAGCTGCGCCATCGGAGGCTGAGAGTTCGCTG 269
Qy 253 ACCCGCGGAGCTCGGCTGCTGCGGGCTGCGGGCTCAGAGCCGCTCGCACCCGCTCC 312
Db 270 AACCGCGGAGCTCGGCTGCTGCGGGTTCGCGGGTTCGCGGGTTCGAGCCGCTCGTACCG-- 325
Qy 313 GACTCCGTCGAAGAAATCGTCCGAGGTCATGAAATCTCGCAAACTCCGTTGACGAAG 372
Db 326 --CTCGTGGGAAGAAATCATCCGAGGTCATGAAATCTTGCATTAATCTCGTTGACGAAG 383
Qy 373 CTCTCTGTTGAAGAGAAATCAGAAAGATTTCTGTTCTTCTTGAACGGGAGGTGATTT 432
Db 384 CTCTCTGTTGAAGAGAAATCAGAAAGATTTCTGTTCTTCTTAAACGGGAGGTGATTT 443
Qy 433 ACCTAGTAGGATGATGGGTTCTGGAAGAAAGTACTGTGGGGAAGATTAATGTCGAAGTCT 492
Db 444 ACTTAGTGGGAATGATGGGTTCTGGAAGAAAGTACTGTGGGGAAGATTAATGTCGAAGTCT 503
Qy 493 TGGGTTATTCGTTCTTTTGTATGATGACAAAGTTAGTGGAGCAAGCTGTGGAATGCCATCAG 552
Db 504 TGGGTTATTCGTTCTTTTGTATGATGACAAATAGTGGAGCAAGCTGTGGAATGCCATCAG 563
Qy 553 TTGCCAAATATTCAGAGTCCATAGTGAAGCCTTTCTTGGGATTAATGAGAGTAGTGTCT 612
Db 564 TTGCTCAAAATATTCAGAGTTCACAGTGAAGCCTTTCTTGGGATTAATGAGAGTAGCGTCT 623
Qy 613 TGAGAGATTTGCTCCATGCGAGCAGTTAGTTGTTGCCACCGGAGGTGCTGTTATCC 672
Db 624 TGAGGAGTGTGCTTCCATGCGACGATTAAGTTGTTGCCACCGGAGGTGCTGTCATCC 683
Qy 673 GACCAATTAAGTGGAGATTAATGAAGAGGCGCTATCTGTTGGTTAGATGTGCCCTTGG 732
Db 684 GACCAATTAAGTGGGAATTAATGAAGAGGCGCTATCCGTTTGGTTAGATGTGCCCTTGG 743
Qy 733 ATGCTCTTGTAGGCGTATTCGTAAGTGGGAATCGCCTCTCGTCTCTTCTTGGACCAAC 792
Db 744 ATGCTCTTGTAGGCGATTCGTAAGTGGGAATCGCCTCTCTCTCTTCTTGGACCAAC 803
Qy 793 CATCTGGTGTATCCGTAAGGATGGGCTTTCTTAAGCTCAGCATGCTTGACGCAAGGG 852
Db 804 CGTCCGGTGTATCCATACAAATGGGCTTTTCTTAAGCTCAGCATGCTTGACGCAAGGG 863
Qy 853 GTGATGCTTATGCAATGCGAGTGAAGGTTTCTCTGGAAGAGATTTGATGTAAACAAG 912
Db 864 GTGATGCTTATGCAATGCGAGTGAAGGTTTCTCTGGAAGAGATTTGATGTAAACAAG 923
Qy 913 GTCATGATGATGCTCTTAAGCTGACACCTTCTGATTAATGCAATTCAGTTCATTAAGA 972


```
RESULT 10
US-10-660-226-27
; Sequence 27, Application US/10660226
; Publication No. US20040064848A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Rendina, Alan
; TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
; FILE REFERENCE: BB-1159-C
; CURRENT APPLICATION NUMBER: US/10/660,226
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/09/354,501
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 27
; LENGTH: 1061
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-660-228-27

Query Match      47.8%; Score 574; DB 18; Length 1061;
Best Local Similarity 81.5%; Pred. No. 4.1e-147;
Matches 693; Conservative 0; Mismatches 145; Indels 12; Gaps 2;

QY 227 GCCACCGGAGCTGAGAGTGCCTGACCGCGGGGACCTGCGTGCCTGCGGGCTCG 286
DB 1 GCACGAGGTGAGCTTCCGTGTGATGATCTGTGTGGGTGCGCGCGCGCTCGCGCG 60
QY 287 CGGGTCCAAAGCCGTCGACCGCTCGACTCCGTGCGAAGAAATCGTCGGAGGTCA 346
DB 61 CGGGCCAAAGCCGCTGCTCCGCTCCG---CGCAAGAAATCGTCTGGAGGAGGTCA 117
QY 347 AAATCGCAACATCCGTTGACGAAGCTCTCTCTGTTGAAGAGAAATCAGAAAGATTCT 406
DB 118 GAATTTGCATACTCGTTGACGATGCCCTCTGTTGAAGAGAAATCAGAAAGATTCT 177
QY 407 GTTCTACTTGAACGGAGGTGATTTTACCTAGTAGAATGATGGGTTCTGGAAAAAGTAC 466
DB 178 TTTCCAGTTGAACGGTCGGTGCATCTACCTAGTTGGAATGATGGGTTCCGGGAAAAGTAC 237
QY 467 TGTGGGGAAGATTATCTCTGAAGTCTTGGGTTATTCTGTTCTTGTAGTGACAAGTTAGT 526
DB 238 GGTGGGGAAGATCTTGCGTGAAGTTTGGGTTATTCTTCGACAGTGATAAATTGGT 297
QY 527 GGAGCAAGCTGTTTGAATGCAATCAGTTGCCCAAAATATTTCAAGGTCATAGTCAAGCCTT 586
DB 298 CGAACAAGCTGTTGGCATGCTTCAAGTGTCTCAAAATTTTCAAGGTTTCAAGTGAAGCCTT 357
QY 587 CTTTCCGGATATGAGAGTAGTGTCTTGAGAGATTTGTCTCTCCATCGCAGATGATTTGT 646
DB 358 CTTTCAAGATATGAGAGTAGTGTCTTGAGGATTTGTCTCAATCGCGCGATGATTTGT 417
QY 647 TGCACCGGAGGTGTGTTTATCCGACCAATTAACCTGAGATATATCAAGAGGGGCT 706
DB 418 TGCTACTGAGGTTGGTCTGTTATCCGACAGTTAACTGGAAAAATATCAAGAGGGGCT 477
QY 707 ATCTGTTTGGTATGATGTGCCCTTGGATGCTCTTGCTAGGCGTATTGCTAAAGTGGGAAC 766
DB 478 ATCTGTTTGGTATGATGTGCCCTTGAAGCTCTTGCAAGCGGTATTGCTAAAGTGGGAC 537
QY 767 TGCCTCTGCTCTCTTTCGACCAACCATCTGGTGTATCCGTAGCGAATGCCCTTTTCTAA 826
DB 538 TGCCCTCGCTCTCTTCTAGATCAACCATCCGCTGATCATACAAATGCGCTTTTCGAA 597
QY 827 GCTCAGCATGCTTGACAGCAAGGGGTGATGCTTATGCAATATGCAGATGTAAGGGTTTC 886

RESULT 11
US-10-739-930-4532
; Sequence 4532, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 4532
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER25671_1
US-10-739-930-4532

Query Match      30.8%; Score 370; DB 20; Length 1223;
Best Local Similarity 64.3%; Pred. No. 6.1e-91;
Matches 606; Conservative 0; Mismatches 325; Indels 11; Gaps 3;

QY 144 ATGAGAGCGGGGGCGTTCGGCTCGCGTTCGAGGGCGGGCGGGGCTTCGGCTCCAGC 203
DB 87 AGGCGCGCGCGCGCTGCTCCCGCACCGAGTCGAGGCGCGGGGCGCTCGCGCTGCAGT 146
QY 204 CGGCACCGGGCGGCTTACAGCGCCACCGGAGCCTGAGAGTCGCTGACCCCGCGGGA 263
DB 147 GCGGGCGCGCGGGGACCGGGCGCGGGCGGGGCGGGGCGGGCGCGCGCTCGGG 206
QY 264 CCGTGGTTCGCTGTCGGGGCTCGGGGTCGCGGCTCGCACCGGCTCCGACTCCGCTCG 323
DB 207 GCGCGCGCGCGGGGCTTCGGGCTCCAGCGCGTCCGCGCGCGCGCGCGCGCGCGG 266
QY 324 AAGAAATCGTCGGAGGTGATGAAAACTCGCACAACTCGGTTGAGCAAGCTCTCTGTTG 383
DB 267 CCCTCGGAGGCGCGCGGCGGCGAGTCCGACGCTCTGCTGCGTCTGCTGACCTCGAGG 326
QY 384 AAGAAAAATCAGAAAGATTCTGTTCTACTTTGAACGGGAGGTGATTTTACTAGTAGA 443
DB 327 GTCTTCAGAGTTGC-----CGGTCTCAATTGAATGGGCCCTCTAGCTACAGAGAGAG 380
QY 444 ATGA--TGGGTTCTGAAAAAGTACTGTGGGGAAGATTATGTTCTGAAGTCTTGGGTTATT 501
DB 381 CTGAAGTGGGCCCTGTAAAGACCGGGCGTGTGATATTCGCCGTTGATTTGGGTTGGGTT 440
QY 502 GCTTCTTTGATGATGACAAAGTTAGTGGAGCAAGCTGTGGTATGCGCATCAGTTGCCCAA 561
DB 441 CATACTTGGACATGATGATTTGGTGAACAGGCGAGTCGGAATGCTTCCGTTGCTCAA 500
QY 562 TATTCAAGTCCATAGTGAAGCCTTCTTTTCGGGATAATGAGAGTAGTGTCTTTGAGAGATT 621
```


Db 501 TATTCAGAGTTACAGTGAAGCAATTTTCAGAGACAGTGAAGTAGTGTCTTCAGAGATT 560
QY 622 TGCTCTCCATCGCAGCAATTAAGTTGTTGCCACCGAGGTGCTGCTGTTATCCGACCAATTA 681
Db 561 TATCCTCAANTCGATCGCTAGTTGTTGCTACTGGAAGCGGTGCTGTTATTCGACCAATT 620
QY 682 ACTGGAGATATGAAGAGGGGCTATCTGTTTGGTTAGATGCGCCTTGGATGCTCTTG 741
Db 621 ACTGGAGATATGAAGAAAGGCTGCTATATCATGTTGGATGTCCTTTGGATGCACTTG 680
QY 742 CTAGGGCTATTGCTTAAGTGGGAACTGCCTCTGCTCTCTCTGGACCAACCATCTGGTG 801
Db 681 CGAAGCGCATGACAAAGTTGGAGCTGCTTCTCGGCCCTTCTAGATCAGCCATCTGCTG 740
QY 802 ATCCGTACCAATGGCCCTTTCTTAAGCTCAGCATGCTTGACAGCAAGGGGTGATGCTT 861
Db 741 ATCCATACACAGCGGCTTTCACAAACTCAGCTGCTCGTGAGCAAGAGGGGATGCTT 800
QY 862 ATGCAAAATGAGATGAAGGTTTCTCTGGAAGAGATTGCAATTAAGCAAGGTCATGATG 921
Db 801 ATGCAAAACCGCATGAAGGTTTCTCTTGAAGAGCTTGCAAGTAAAGGGTCAATGATG 860
QY 922 ATGCTCTAAGCTGACACCTACTGATATTGCAATTTAGTCACTTCAATAGATCGAGCT 981
Db 861 ATGCTCTCAGCTTAACCCCACTGATATTGCTGTCAGGGCCCTTACAAAGATTGAAGATT 920
QY 982 TCGTCACTCGAGCA--CACTGCTGATAGTTTCAGTACGACGCGCAAGCTGAGTCCGAGA 1038
Db 921 TTGTCAGTACGATTCATGCGCCAGTGGCCCATTCGACGACTTATAAATTGGTGCCAGGA 980
QY 1039 TCCAGAGGATACAGACCTTGTAGAACCTTAATCCCTTTGTTT 1080
Db 981 GACCAACGATGCAATCTCTGTAGAAATTTTCAGCCCAATTTGT 1022

RESULT 12
US-10-425-115-68871/c
; Sequence 68871, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 68871
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_162804C.1
US-10-425-115-68871

Query Match 30.6%; Score 367.8; DB 20; Length 1503;
Best Local Similarity 67.3%; Pred. No. 2.7e-90;
Matches 518; Conservative 0; Mismatches 252; Indels 0; Gaps 0;

QY 228 CCCACCGGAGCTGAGATCGCTGACCCCGGGGACCTGCGTGCCTGTGGGGCTCGC 287
Db 1137 CCAGCGGAGGCTCGCGTGGCGGGAGCAGCGCCGGAGGCTGTGCTGTGGCGCC 1078
QY 288 GGGTCCAAAGCCCGTCGACCGCTCCGACTCCGTCGGAAGAAATCGTCCGAGGTCATGAA 347
Db 1077 GATACGCGGAGGCGCGGATCTGCGCTCGTGGCGCGCAATCTCAGGAAACAGGA 1018
QY 348 AACTCCGACAACTCCGTTGACGAAGCTCTCCTGTTGAAGAGAAAAATCAGAAAGTTCTG 407

Db 1017 AAGGTCCACTACTCTGCTGATGACGCTCTCATACTACAGCAAAAGCCAGGATGTTCTG 958
QY 408 TTCTACTTGAACGGAGGTGTAATTTACCTAGTAGGAAATGATGGGTTCTGGAANAAGTACT 467
Db 957 CTTTACTTGGATGGCCGTTGCGTTTATCTTTGGNAATGATGGGTTTCAGCAAAACTACA 898
QY 468 GTGGGGAAGATTATGCTGAAAGCTTTGGGTTTATTCGTTCTTTGATAGTCAAGTTAGTG 527
Db 897 GTTGGGAAGATACTATCCGAAGTGTAGGTTATTCGTTCTTCACACAGTATAAGTTGGTA 838
QY 528 GAGCAAGCTTTGGATGCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 587
Db 837 GAGAAGGCTGTTGGTATTTTCATCTGTTGCTGAGATCTTTTCAGCTCCATCGGAAACATT 778
QY 588 TTTCCGGATAATGAGAGTAGTGTCTTGGAGAGATTTGCTCTCCATGGAGCATTTAGTTGTT 647
Db 777 TTCAGAGATATGAGAGTAGGAGTCTGAGGATCTGTCAATCAATGATCGGTTGGTTGTT 718
QY 648 GCCACGGAGGTGCTGCTTTATCCGACCAATTAATCGAGATATATGAAGAGGGGCTTA 707
Db 717 GCAACCGGAGGTGCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 658
QY 708 TCTGTTGTTAGATGTCCTTGGATGCTCTTCTGCTAGGCTTATTCGTAAGTGGGAACT 767
Db 657 ACCGTATGGTTAGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 598
QY 768 GCTCTGCTCTCTTCTGGACCAACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 827
Db 597 GGGTCTCGACCACTTTCGATCAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 538
QY 828 CTCAGCATGCTTCGACAGCAAGGGGTGATGCTTATGCAAAATGCAAAATGCAAGTGAAG 887
Db 537 CTTACATCACTTTTTCGACCAAGAAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 478
QY 888 CTGGAAGAGATTGCAATGTAACAGGTCAATGATGATGCTCTTAAGCTGACACCTACTGAT 947
Db 477 CTTGAACATATTGCAATTAACCAAGGCCAATAATGATGTCATATATCTTACACCTAGTACC 418
QY 948 ATTGCAATGAGTCACTTTCATTAAGATCGAGAGCTTCTGCTCATCGAGCACAC 997
Db 417 ATCGCATGAGGCATTGCTAAAGATGGAAGTTTCTTACCGAGAGAGAC 368

RESULT 13
US-10-660-226-25
; Sequence 25, Application US/10660226
; Publication No. US20040064848A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Lavo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Rendina, Alan
; TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
; FILE REFERENCE: BB-1159-C
; CURRENT APPLICATION NUMBER: US/10/660,226
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/09/354,501
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-660-226-25

Query Match 30.4%; Score 364.4; DB 18; Length 1323;
Best Local Similarity 71.9%; Pred. No. 2.2e-89;
Matches 476; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

333	TCCGGAGGCTCATGAAACCTCGCACAACCTCCGTTGACGAAGCTCTCTCTGTTGAAGAGAAA	392
Qy		
170	TCGGCAGGTAAGTCTGCTTCTACCTTTGAAACGGGAGGTGTAATTTACCTAGTAGCAATGATGGGT	452
Db		
393	TCAGAAAGAGTTCTGTTCTTCTACCTTTGAAACGGGAGGTGTAATTTACCTAGTAGCAATGATGGGT	452
Qy		
230	GCAGAGACGTGCTCCCTTTACCTGAAATGACCGCTGTGTTTATCTAGTTTGAATGATGGGT	289
Db		
453	TCTGSAAGAGTACTGTGGGGAAGATTATGTCTGAAAGCTTTGGGTATTATTCGTTCTTTGAT	512
Qy		
290	TCCGGCAAAACTACAGTTGGGAAGATAATAGCTGAAGTACTAGGCTATTCTTCTTTGAC	349
Db		
513	AGTGACAAGTTAGTGGAGCAAGCTGTCGGAATGCCATCAGTTCGCCAAATATTCAAGGTC	572
Qy		
350	AGTGATAAGCTGGTTGAGCAGTCTCTGTGGCATACCGTCGGTGGCTGAGATTTTTTCAGGTC	409
Db		
573	CATAGTGAAGCCCTCTTTCCGGGATAATGAGAGTAGTGTCTTTGAGAGATTTGTCTCCTCATG	632
Qy		
410	CACAGTGAAGCATTTCTTCAGAGATAACGAGAGTGAGGTACTAAGGGATTTTGTGTCAAATG	469
Db		
633	CGACGATTAGTTGTTGCCACCGGAGGTGGTGTGTATCCGACCAAATTAATCTGGAGATAT	692
Qy		
470	CACCGAATAATTGTTGCCAACGAGAGGTGGTGGGTGATACGACCAATCAATTGGAGTTAT	529
Db		
693	ATGAAGAGGGGCGCTATCTGTTGGTTAGATGTGCCCTTGGATGCTCTTGTCTAGGCGGTATT	752
Qy		
530	ATGAAGAAAGGACTCACTATTTTGGTTAGATGTTCCATTGGACGCCCTTGAAGAAGGATT	589
Db		
753	GCTAAAGTGGGAACCTGCTCTGCTCTCTTCTGGACCAACCATCTGTGTGATCGTAGGCA	812
Qy		
590	GCTGCGGTTGGTACTGCGTCACGACCCCTCTGCAATCAGGAATCTGTGTATCTCTTATGCA	649
Db		
813	ATGGCTCTTTCTTAAGCTCAGCATGCTGTGCACAGAAAGGGGTGATGCTTATGCAAAATGCA	872
Qy		
650	AAGGCTATGCCAAACTTACAGCACTTTTGNACAAAGATGGATTCAATGCTAATGCT	709
Db		
873	GATGTAAGGGTTTCTCTGGAAGAGATTTGCATGTAAACAAAGGTCAATGATGATCTCTAAG	932
Qy		
710	GATGCGCGAGTTTCCCTTGAAATAATTTGCATTCAACAAAGGACATAATGATGTGAATGTA	769
Db		
933	CTCACACCTTACTGATATTCGAATTGAGTCACTTTCATTAAGTCGAGAGCTTCGTCATCGAG	992
Qy		
770	CTTACACCAAGTCCCATCGCTATTGAGGCAATTGCTTAAGATGGAGAGCTTCTTACTGAG	829
Db		
993	CA 994	Qy
830	AA 831	Db

RESULT 14

US-10-660-226-11 ; Sequence 11, Application US/10660226 ; Publication No. US20040064848A1

GENERAL INFORMATION: 60/093,611
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Hitz, William D.
APPLICANT: Rendina, Alan
TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
FILE REFERENCE: BB-1159-C
CURRENT APPLICATION NUMBER: US/10/660,226
CURRENT FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US/09/354,501
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,611
PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 11
LENGTH: 899
TYPE: DNA
ORGANISM: Zea mays

US-10-660-226-11

Query Match 30.3%; Score 363.4; DB 18; Length 899;
Best Local Similarity 71.0%; Pred. No. 3.4e-89;

QY	321	CGAAGAAATCGTCCGGAGGTCTGAAAACTCGCAAACTCGTTCGTTGACGAAGCTCTCTCGT	380
DB	5	GAGCGCAATCTCGCAGGTGGAAACGGAAGAAGTCCACTACTCTGCTGATGAOCGCTCTCATTA	64
QY	381	TTGAAGAGAAAATCAGAAAGAAGTCTGTCTTACTTGAACGGGAGGTGTAATTACCTAGTA	440
DB	65	CTACAGCAAAAAGCCAGGATGTTCTGCCTTACTTTGGATGSCCGTTGCGTTTATCTTGTT	124
QY	441	CGAATGATGGGTTCTGGA AAAAGTA CTGTGGGGAAGATTA TGTCGTGAAGTCTTTGGGTTAT	500
DB	125	CGAATGATGGGTTCAAGGCAAACTACAGTTGGGAAGATACTATCCGAAAGTGTGAGTTAT	184
QY	501	TCGTTCTTTGATAGTGACAAGTATGTGAGCAAGCTGTTGGAATGCCACTCAGTTGCCAA	560
DB	185	TCGTTCTTCGACAGTGATAGTTGGTAGAAGGCTGTTGGTATTTCATCTCTGTTGCTGAG	244
QY	561	ATATTC AAGGTC CATAGTGAAGCCCTCTTTCCGGATAATGAGAGTAGTGTCTTGAGAGAT	620
DB	245	ATCTTTCAGCTCCATAGCGAAACA TCTTCAGAGATAATGAGTAGAGTCTCTGACGGAT	304
QY	621	TTGTCTCCATGCGACGATATAGTTGTTGCCACCGGAGGTGGTCTGTTATCCGACCAATT	680
DB	305	CTGTCATCAATGCATCGGTGGTGTGTC AACC GGAGGTGGTGCAGTGATCCGACCAATC	364
QY	681	AACTGGAGATATGAAGAGGGGCCATCTCTGTTTGGTTAGATGTGCCCTTGGATGCTCTT	740
DB	365	AATTGGAGTTACATGAAGAAAGGGCTGACCGTATGTTTAGATGTCCCACTGGATGCAC TT	424
QY	741	GCTAGCGGTATTGCTAAAGTGGGAACTGCGCTCTCGTCTCTTCTGGA CCAACATCTGCT	800
DB	425	GCAAGAAAGATCGCTGCTGTAGGAACCGCGTCTCGACCAC TCTTGCA TCAGGAATCCGCT	484
QY	801	GATCCGTACGCAATGGGCCCTTTTCTAAGCTCAGCATGCTTGCA CAGCAAGGGGTGATGCT	860
DB	485	GATCCTTATGCNAAGGCTTATGCCAAA CTTACGTCACTTTTGTAGCAAGAATGGACTCG	544
QY	861	TATGCAAAATGCAGATGTAAGGGTTTCTCTGGAAGAGATTGCATGTATAACAAGTCAATGAT	920
DB	545	TATGCTAATGCTGATGCCAGAGTTTCACTTGAACATATTTGCATTAAAAACAAGGCCATAAT	604
QY	921	GATGTCCTTAAGCTGCACACCTACTGATATTGCAATTTGAGTCACTTTCATAAGATTCAGAGC	980
DB	605	GATGTCATCTACTTACACCTAGTACCATTGAGCCATTGAGGCATTGCTAAAGATGGAAGT	664
QY	981	TTGCTCATCGAGCACAC	997
DB	665	TTTCTTACCGAGAC	681

RESULT 15

US-10-660-226-19 ; Sequence 19, Application US/10660226
: Publication No. US20040064848A1

GENERAL INFORMATION: REBECCA E. CAHOON
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Hitz, William D.
APPLICANT: Rendina, Alan
TITLE OF INVENTION: Chromatate Biosynthesis Enzymes
FILE REFERENCE: BB-1159-C
CURRENT APPLICATION NUMBER: US/10/660,226
CURRENT FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US/09/354,501
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: EARLIER
PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
60/093,611

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; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Sorghum
US-10-660-226-19

Query Match      30.2%; Score 362.6; DB 18; Length 960;
Best Local Similarity 71.6%; Pred. No. 5.8e-89;
Matches 476; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 333 TCCGGAGGTCATGAAGAACTCGACAACTCGGTGACGAGCTCTCTGTTGAAGAGAAA 392
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
59 TCGGCAGGAACAGGAAAGTCCACTATTCTACTGACGAGGCTCTCATCTACAGCAAAAG 118
QY 393 TCAGAAAGAGTTCTGTTCTACTTTGAACGGGAGGTGTATTACCTAGTAGGAATGATGGGT 452
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
119 GCCCAGATGTTCTCCCTTACTTTGGATGGCCGATGGGTTTATCTGTTGGAATGATGGGT 178
QY 453 TCTGGAAGAAAGTACTGTGGGGAAGATTATGCTCTGAAGTCTTGGGTTATTTCGTTCTTTGAT 512
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
179 TCAGGCAAACTACAGTTGGGAAGATATTAGCCGAAAGTATTAGGTTATTTCGTTCTTTGAC 238
QY 513 AGTGACAAGTTAGTGAGCAAGCTGTGTGGAATGCCATCAGTTGCCCAAATATTCAAGGTC 572
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
239 AGTGATAAGCTGTAGAGAAGGCTGTGGTATCTCATCTGTTGCTGAGATCTTTTCAGCTC 298
QY 573 CATAGTGAAGCTTCTTTCGGGTAATGAGAGTAGTGTCTTGAGAGATTGTCTCTCATG 632
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
299 CATAGTGAAGCATTTCTTACAGAGATATGAGAGTGAGGTCTGAGGATCTGTCAATCAATG 358
QY 633 CGACCGATTAGTTCTTGCCACCGAGGTGGTGTCTGTTATCCGACCAATTAACTGGAGATAT 692
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
359 CATCGGTGTTGTTGCAACCGAGGTGGTGCAGTGTCCGACCAATCAATTGGAGTTAC 418
QY 693 ATGAAGAGGGGCTATCTGTTGTTGTTAGATGTGCCCTTGATGCTCTTGCTAGGCGTATT 752
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
419 ATGAAGAAAGGGCTGACTGTGTGTTAGACGTTCCACTGCGATGCACTTGCAAGAGAAAT 478
QY 753 GCTAAAGTGGAACTGCCTCTGCTCTCTTCTGGACCAACCATCTGGTATCGGTACGCA 812
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
479 GCTGCTGTAGGAACCGCATCTCGACCACCTTTGCAATCAGGAATCTGGTGACCCCTTATGCA 538
QY 813 ATGGCCTTTTCTAAGCTCAGCATGCTTGCAACAAAGGGGTGATGCTTATGCAAAATGCA 872
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
539 AAGCTTATCGGAACCTTACATCACTTTTGGACAAAGAAATGGACTCGTATGCTAATGCT 598
QY 873 GATGTAAGGGTTTCTCTGGAAGAGATTGCATGTAAACAAAGGTCAATGATGTCTCTAAG 932
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
599 GATGCCAGAGTTTCACTTGAACATAATTGCATTAAACNAAGGCCATAATGATGTCACTATA 658
QY 933 CTGACACCTACTGATATTGCAATTGAGTCACTTCAATAGATCGAGAGCTTCGTCATCGAG 992
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
659 CTTACACCTAGTGCCCATCGCCATTGAGGCATTGCTAAAGATGGAAGTTTCTTACCGAG 718
QY 993 CACAC 997
Db      |||
719 AAGAC 723
```

Search completed: August 25, 2005, 20:43:27
Job time : 890 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2005, 14:05:03 ; Search time 4422 Seconds
(without alignments)
10329.517 Million cell updates/sec

Title: US-10-660-226-9

Perfect score: 1200

Sequence: 1 ccgccaccagctaccctgcc.....aaaaaaaaaaaaaaaaaaaaa 1200

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	824	68.7	1305	3	AY104682	Zea mays
2	619.8	51.6	804	7	CN147205	WOUND1_48
3	610.6	50.9	667	6	CA078453	SCRLAM100
4	567.6	47.3	672	6	CA146167	SCVPR1207
5	566	47.2	582	5	BQ577650	3524_1_39
6	566	47.2	825	6	CB684025	OSJNEf13C
7	549	45.8	549	7	COS24949	3530_1_16
8	547.8	45.6	619	6	CA452817	RP3A1_3_H0
9	546.6	45.6	833	6	CB657302	OSJNEc11
10	542	45.2	609	2	AW671996	LGI_353_A
11	540.8	45.1	620	6	CF033002	QCf11b08.
12	537.2	44.8	814	7	CF636791	zmrmw00.0
13	530.8	44.2	650	6	CA105686	SCJFHR1C0
14	524	43.7	728	7	CN144547	WOUND1_23
15	520.8	43.4	818	6	CB684026	OSJNEf13C
16	516.4	43.0	809	6	CB656619	OSJNEc11D
17	513	42.8	854	6	CB657303	OSJNEc121
18	510.4	42.5	775	6	CA182703	SCEZST314
19	508.8	42.4	701	7	CN144633	WOUND1_23
20	506.2	42.2	733	6	CA452716	RP3A1_1
21	505.2	42.1	789	6	CB656559	OSJNEc11B
22	505	42.1	797	6	CB641679	OSJNEb01H
23	503	41.9	504	7	COS19743	3530_1_13
24	502.6	41.9	659	6	CA112411	SCEQDB106

c	25	502.4	41.9	789	6	CB656620	OSJNEc11D
	26	500.8	41.7	582	4	BG355018	BG355018
	27	497.8	41.5	640	4	BJ472228	BJ472228
	28	496.8	41.4	689	4	BJ248029	BJ248029
	29	496.4	41.4	612	6	CA118037	SCBGR104
	30	495	41.2	642	6	CD670151	3529_1_12
	31	493.6	41.1	786	7	CK827364	zmrmw00.0
	32	492.4	41.0	586	7	COS24948	3530_1_16
	33	491.2	40.9	772	6	CB656558	OSJNEc11B
	34	490.2	40.8	601	1	AI795555	614009G01
	35	488.6	40.7	504	7	COS19742	3530_1_13
	36	484.2	40.3	669	6	CA248324	SCCCFL509
	37	483.8	40.3	604	2	BE593776	WSI_102_A
	38	482.4	38.1	914	4	BG301287	HVMSB002
	39	455.8	38.0	670	7	CF633545	zmrmw00.0
	40	455.6	38.0	513	2	AW671997	LGI_353_A
	41	450.6	37.5	649	1	AV909303	AV909303
	42	450.4	37.4	649	7	CF489674	POLL_59_A
	43	448.2	37.4	619	4	BG241548	RHI22_51
	44	446.4	37.2	711	6	CA137983	SCEPRT204
	45	435.4	36.3	1066	7	CR286591	CR286591

ALIGNMENTS

RESULT 1	AY104682	1305 bp	mRNA	linear	HTC 16-OCT-2002
LOCUS	AY104682				
DEFINITION	Zea mays PCO108968 mRNA sequence.				
ACCESSION	AY104682				
VERSION	AY104682.1	GI:21207760			
KEYWORDS	HTC.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whiteaitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.				
TITLE	Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes				
JOURNAL	Unpublished (2002)				
REFERENCE	2 (bases 1 to 1305)				
AUTHORS	Coe,E.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA				
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.				

FEATURES

source	1..1305
Location/Qualifiers	/organism="Zea mays"
	/mol_type="mRNA"
	/db_xref="MaizeDB:636337"
	/db_xref="taxon:4577"
	/clone_lib="Maize Mapping Project/DuPont Consensus Library"
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 68.7%; Score 824; DB 3; Length 1305;

Qy	15	CCTGCCCTCTCTCTCTCTCTCTCTTTACACCTCACCTCCGGATCGCTCAGAGAGTCAG--AG	72
Db	66	CCTGCCCTCTGCCCTCTCCCTCTGTTTTCTAGACCCCGGATCGCTCAGAGATTGAGTCGT	125
Qy	73	ATTCCGAGTTGAGCTATAGGCGTAGCCGATGGTCGCGCGTCCCTCTCGGCTCCACCG	132
Db	126	AGTCGTACCGACTAGTCGCGCGTCTCTTTCCCGCGCAGCAGCAGCACCACCG	185
Qy	133	GCAGAGCAACAAATGGAGCGGGGGCGTCGCGCTTGGCGCTGCAGGCGCGGCGCGGCT	192
Db	186	GTGACGAGCAATGGAGCGGGGGCGTGGGCTTGGCGCTGCACACGCGGCGCGGCGCT	245
Qy	193	TCGGCTCAGCGGCAACGCGGGGGCGCTACAGGCGGCCCAACGCGAGCCTGAGAGTCGCTG	252
Db	246	TCGGCTCCGCGCAGCGCGGGGGCGCTACAGTCGCGCCATCGGAGAGCTGAGAGTCGCTG	305
Qy	253	ACCGGGGGACCTGCGGCTCGCTGCGGGCTCGCGGCTCAAGCCCGTCGACCGCTCC	312
Db	306	AAACCGGGGGAGCTGCGGTTGCGGTGCGGGTCCAGCCCGTCGTACCG----	361
Qy	313	GACTCCGTGCGAAGAAATCGTCGGAGGTCATGAAAACTCGCAACATCCCGTTGACGAAG	372
Db	362	--CTCCGTGCGAAGAAATCATCGGAGGTCATGAAAACTTGCAATACTCCGTTGACGAAG	419
Qy	373	CTCTCCTTTGAGAGAGAAATCAGAGAAAGTCTGTTCTACTTGAAACGGGAGGTGATTT	432
Db	420	CTCTCCTTTGAGAGAGAAATCAGAGAAAGTCTGTTCTACTTAAACGGGAGGTGATTT	479
Qy	433	ACCTAGTAGGAATGATGGGTTCTGAAAAAGTACTGTGGGAAAGATTATGTCTCAAGTCT	492
Db	480	ACTTAGTGGAAATGATGGGTTCTGAAAAAGTACTGTGGGAAAGATCATGTCTGAAGTCT	539
Qy	493	TGGGTTATTGTTCTTTGATAGTACAAAGTTAGTGGAGCAAGCTGTGGAAATGCCATCAG	552
Db	540	TGGGTTATTGTTCTTTGATAGTACAAATTTAGTGGAGCAAGCTGTGGAAATGCCATCAG	599
Qy	553	TTGCCCAAAATTTCAAGTCATAGTGAAGCTTCTTTTCGGGATAATGAGAGTAGTGTCT	612
Db	600	TTGCTCAAAATTTCAAAAGTTTCAAGTGAAGCTTCTTTTCGGGATAATGAGAGTAGTGTCT	659
Qy	613	TGAGAGATTGTCTCTCAACGACGATTAGTTGTGGCACCGAGGTGGTCTGTTATCC	672
Db	660	TGAGGGAATCTGTCTCTCAACGACGATAGTTGTGGCACCGGA--GTTGCTTGTCTATCC	718
Qy	673	GACCAATTAATCGAGATATATGAAGGGGCTTATCTGTTGGTTAGATGTGCCCTTGG	732
Db	719	GACCAGTTAACTGGAATATATGAAGAAGGSCCTATCCGTTTGGTTAGATGTGCCCTTGG	778
Qy	733	ATGCTCTTGCTAGGCGTATTGCTAAAGTGGGAACTGCGCTCTGCTCCTTCTTGACACCAAC	792
Db	779	ATGCTCTTGCTAGGCGATTTGCTAAAGTGGGAACCGCTTCTCGTCTCTTCTTGACCAAC	838
Qy	793	CATCTGTGTATCCGTAGCGAATGCCCTTTTCTAAAGCTCAGCATCTTTGCACAGCAAAAGG	852
Db	839	CGTCCGGTGATCCATACAAATGSCCTTTCTAAGCTCAGCATGCTTGCAGCAAAAGG	898
Qy	853	GTGATGCTTATGCAAAATCGAGATGAAGGGTTCTCTGGAAGAGATTGCATGTAAACAAG	912
Db	899	GTGATGCTTATGCAAAATCGGATGTAAGGGTTCTCTGGAAGAGATTGCATGTAAACAAG	958
Qy	913	GTCAATGATGTCCTTAAGCTGACACCTACTGATATTGCAATTTGAGTCACCTCATTAAGA	972
Db	959	GTCAATGCGGATGTCCTTAAGCTGATGCGGACTGATATCGCAATTTGAGTCACCTCATTAAGA	1018
Qy	973	TCGAGAGCTGCTCATCGAGCACACTGCTGATAGTTCAGCTAGCGAGCGCGCAAGCTGAGT	1032
Db	1019	TCGAGAGTTTCTCATCGAGCACCTGCTGATTAATTCAGCTAGCGACTCGCAAGCTGAGT	1078
Qy	1033	CGCAGATCCAGGAGTACAGACTTGTAGAACCTTAAATCCCTTTGTTGGCAAC	1085

Db	1079	CACAGATCCAAAGGATACAGACCTTGCTAATATCTTAATCCTCTGTTTGTAC	1131
RESULT 2			
CN147205			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 700; Conservative			
Qy	412	ACTTTGACCGGAGCTGTATTACCTAGTAGGAATGATGGTCTCTGGAAAAGTACTCTGG	471
Db	1	ACTGTGACCGGAGGTGTATTATCTTAGTAGGAATGATGGTTCTGGAAAAGTACAGTGG	60
Qy	472	GGAAAGATTATGTCCTGAAGTCTTCGGGTATTTCGTTCTTTTGTAGTAGTGAACGTTAGTGGAGC	531

Db	61	GGAAAGATTATGCTGAAAGCTTGGGTATTTCGTTCTTTGACAGTGCACAAATATTAGTGGAGC	120
Qy	532	AAGCTGTTGGAAATGCCATCAGTTCGCCAAAATATTCAAGGTCCTAGTAGTGAAGCCCTTCTTTTC	591
Db	121	AAGCTGTTGGAAATGCCCTTCAGTTCAGTTCCTCAAAATATTCAAGGTTTCATAGCGAAGCCCTTCTTTTC	180
Qy	592	GGGATAATGAGAGTAGTGTCTTTGAGAGATTTGTCTCTCATCGAGAGATATTAGTTGTTGGCA	651
Db	181	GGGATAATGAGAGTAGTGTCTTTGAGAGATTTGTCTCTCATCGAACGATATTAGTTGTTGGCA	240
Qy	652	CCGAGGTGGTGTGTTTATCCGACCAAATTAACCTGGAGATATATGAAGAGGGCCCTATCTG	711
Db	241	CCGCGGTGGTGTGTTTATCCGACCAAGTAACTGGAAATATATGAGAGAGGGCCCTATCTG	300
Qy	712	TTTGGTTAGATGTGCGCCTTGGATGCTCTTGTCTAGCGGTATTGCTAAAGTGGGAATCTGCCT	771
Db	301	TTTGGTTAGGTGTGCGCCTTGGATGCTCTTGTCTAGCGGTATTGCTAAAGTGGGAATCTGCCT	360
Qy	772	CTCGTCTCTTCTCGACCAACCATCTGGTGATCCGTACGCAATGGCCCTTTCTTAAGCTCA	831
Db	361	CTCGTCTCTCTCGACCAACCATCTGGTGATCCATACCAATGGCCCTTCTCTAAGCTCA	420
Qy	832	GCATGCTTGCAACAGAAAGGGGTGATGCTTATGCAAAATGCAGATGTAAAGGTTTCTCTCG	891
Db	421	GCATGCTTGACAGACNAAGGGTGAACGCTTATGCAATGCAGATGTAAAGGTTTCTCTAG	480
Qy	892	AAGAGATTGCATGTAAACAAGGTCATGATGATCTCTTAAGCTGACACCTTACTGATATTG	951
Db	481	AAGAGATTGCATCTAAGCAAGGTCACCATGATGTCCTTAAAGCTGACACCCACTGATATCG	540
Qy	952	CAATTGAGTCACTTCATAAAGATCGAGAGCTTCGTCATCGACGACACATGCTGATAGTTGAG	1011
Db	541	CAATTGAGTCACTTCATAAAGATCGAGAGCTTCGTCAGCGAGCACATCTCGATTAATCCAG	600
Qy	1012	CTAGCGACGCGCAAGCTGAGTCGAGATCCAGAGGATACAGACCTTGTAGAACCTTAATC	1071
Db	601	CTAGCGACTCGCAAGCTGAGTCGAGATCCAAAGGATACAGACCTTGTAGAACCTTGTATC	660
Qy	1072	CTTTTGTGTTG-----CCACATAGAGCATCGTTGAGTTATTGTT--AAAGGAT	1117
Db	661	CTTTTGTGTTGACCGTAGTGTACCACTAGAGCATCGTTGAGTTATTGTTGTTGTCATT	720
Qy	1118	GGAAAGAGGGAGCTAAATAATCCGAAGTGTGCGGTGGCTGAAAAAATAAAAAAAAAAAAA	1177
Db	721	GTACAGAGGGAGGAGAAACCTGAAGCAATTTCTTGTTATAGCTGTAAAGGATGGTAATA	780
Qy	1178	AAAAAAAAAAAA 1188	
Db	781	AGGGAGATAAA 791	

RESULT 3	
CA078453	
LOCUS	667 bp mRNA linear EST 23-SEP-2003
DEFINITION	SCRLAM1007D04.g AM1 Saccharum officinarum cDNA clone SCRLAM1007D04
ACCESSION	5', mRNA sequence.
VERSION	CA078453
KEYWORDS	CA078453.1 GI:34930725
SOURCE	EST.
ORGANISM	Saccharum officinarum
	Saccharum officinarum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
	clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
	complex.
REFERENCE	1 (bases 1 to 667)
AUTHORS	Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE	The libraries that made SUCEST
JOURNAL	Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT	Contact: Arruda P
	Centro de Biologia Molecular e Engenharia Genetica
	Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
<http://www.bcccenter.fcav.unesp.br>
Plate: 007 row: D column: 04
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .667
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCLAM1007D04"
/lab_host="DH10B"
/clone_lib="AM1"
/notes="Organ: Apical meristem and tissues surrounding of
mature plants; Vector: pSport1; Site 1: SalI; Site 2:
NotI; An unidirectional cDNA library generated from
[Apical meristem and tissues surrounding of mature
plants]. cDNA was prepared from polyA+ mRNA using
SuperScript plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CU-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at <http://suicet.lad.ic.unicamp.br/public>"

FEATURES
source

ORIGIN

Query Match	50.9%	Score 610.6	DB 6	Length 667
Best Local Similarity	94.7%	Pred. No. 7.8e-137		
Matches 631	Conservative 0	Mismatches 35	Indels 0	Gaps 0
Qy	340	GTCAATGAAACTCGCAACACTCGTTGTGACCAAGCTCTCTGTTGTGAAGAGAAAATCACAAG	399	
Db	1	GTCAATGAAACTTGCATTAACCTCGTTTGACGAAGCTCTCCTATTGTGAAGAGAAAATCAGAAG	60	
Qy	400	AAGTTCCTGTTCTACTTTGAACCGGAGGTGTATTTTACCTAGTAGGAAATGATGGGTTCTGGAA	459	
Db	61	AAGTCTTGTTCCTACTTTGAACCGGAGGTGTATTTACTTTAGTAGGAAATGATGGGTTCTGGAA	120	
Qy	460	AAAGTACTGTGGGGAGATTTATCTCTGAAGTCTTGGGTTATTCGTTCTTTGTAGTAGTGACA	519	
Db	121	AAAGTACCGTGGGGAGATTTATCTCTGAAGTCTTGGGTTATTCGTTCTTCGATAGTAGACA	180	
Qy	520	AGTTAGTGAAGCAAGCTGTTGGAAATGCCATCAGTTGCCCAAATATTCAAGGTTCCATAGTG	579	
Db	181	AATTAGTGGAGCAAGCTGTTGGAAATGCCTTTCAGTTGCCCAAATATTCAAGGTTTCATAGCG	240	
Qy	580	AAGCCTTTCTTCGGGATAATAGAGAGTAGTGTCTTTGAGAGATTTTGTCTCCTCATCGGACGAT	639	
Db	241	AAGCCTTCTTTTCGGGATAATGAGAGTAGTGTCTTTGAGAGATTTTGTCTCCTCATCGGACGAT	300	
Qy	640	TAGTTGTGTCACCGGAGGTGGTGCTTTATCCGACCAATTAACTGGAGATATATGAAGA	699	
Db	301	TAGTTGTGTCACCGGAGGTGGTGCTTTATCCGACCAAGTTAACTGGAAATATATGAAGA	360	
Qy	700	GGGGCCCTATCTGTTTGGTTAGATGTGCCCTTGGATGCTCTTGTAGSCGTATTGCTTAAAG	759	
Db	361	AGGGACTATCTGTTTGGTTAGATGTGCCCTTGGATGCTCTTGTAGSCGTATTGCTTAAAG	420	
Qy	760	TGGGAACTGCCTCTCGTCTCTTCTGGACCAACCATCTGGTGATCCGTACGCCAATGGCCCT	819	
Db	421	TGGGAACTGCCTCTCGTCTCTTCTGGATCAACCATCTGGTGATCCCATACACAATGGCCCT	480	
Qy	820	TTTCTAAGCTCAGCATGCTTGCACAGCAAAAGGGTGATGCTTATGCAAAATGTCAGATGTAA	879	
Db	481	TTTCTAAGCTCAGCATGCTTGCAGAGCAAAAGGGTGATGCTTATGCAAAATGTCAGATGTCA	540	
Qy	880	GGGTTTTCTCTGGAGAGATTGCATGTAAACAAGGTCATGATGATGTCCTCTTAAGCTGCAC	939	
Db	541	NGGTTTTCTCTGGAGAGATTGCATTTAAACAAGGCCACCATGATGTCCTTTAACTGCACAC	600	

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QY 940 CTACTGATATGCAATTGAGTCACCTTCATAAGATCGAGAGCTTCGTTCATCGAGCACACTG 999
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
601 CCACCTGATATGCAATTGAGTCACCTTCATAAGATCGAGAGCTTCGTTCACGAGCACACTC 660
QY 1000 CTGATA 1005
Db |||||
661 CAAATA 666

RESULT 4
CAL146167 672 bp mRNA linear EST 24-SEP-2003
SCVPR2077B07.g RT2 Saccharum officinarum cDNA clone SCVPR2077B07
5', mRNA sequence.
ACCESSION CAL146167
VERSION CAL146167.1 GI:35044937
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 672)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 077 row: E column: 07
Seq primer: T7 Promoter Primer.
FEATURES
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/organism="Saccharum officinarum"
/mol_type="mRNA"
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/clone="SCVPR2077B07"
/lab_host="DH10B"
/clone_lib="RT2"
/notes="Organ: Root tips(0.3cm-long) from adult plants;
Vector: pSport1; Site 1: SalI; Site 2: NotI; An
unidirectional cDNA library generated from [Root
tips(0.3cm-long) from adult plants]. cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"

Query Match 47.3%; Score 567.6; DB 6; Length 672;
Best Local Similarity 93.5%; Pred. No. 2e-126;
Matches 604; Conservative 0; Mismatches 36; Indels 6; Gaps 1;

QY 130 CCGCGGAGCAACAATGGAGCGGGGGCGTTCGGCTGCGTGCAGCGCGGGCGGCGGCGG 189
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
33 CCGGCGAGCGACCAATGGAGCGGGGGCGTGGGGCTGGCGTGCAGACGCGGGCGGCGG 92
QY 190 GCTTCGGCTCCAGCGGCGGCGGCGCTACAGCGGCGGCGGCGGCGGCGGCGGCGGCTGAGAGTCG 249
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
93 GCTTCGGCTCCAGCGGCGGCGGCGGCGCTACAGTCGCGGCGGCGGCGGCGGCGGCGGCTGAGAGTCG 152

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QY 250 CTGACCCCGCGGGAACCTCGCGTCTGTCGGGGCTCGCGGGTCCAAAGCCCGTCGACCCGC 309
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
153 CTGGCCCGTCGGGAGCAGCGGTGCTGTGCGGGTTCGCGGGTCCAAAGCCCGTCGACCCGC- 211
QY 310 TCCGACTCCGTCGGAAGAAATCGTCCGAGGTCATGAAACTCGCACAACTCCGTTGAGC 369
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
212 -----CTCGTGCGAAGAAATCGTTCGGTGGTTCATGAAAACTTGCAATACTCCGTTGAGC 266
QY 370 AAGCTCTCTCTGTTGAAGAGAAATCAGAAAGATGTTCTGTTCTTACTTTGAACGGGAGGTGTA 429
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
267 AAGCTCTCTCTGTTGAAGAGAAATCAGAAAGATGTTCTGTTCTTACTTTGAACGGGAGGTGTA 326
QY 430 TTTACTAGTAGGAATGATGGTTCGAAAAAGTACTGTGGGGAAGATTATGTTCTGAAG 489
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
327 TTTACTAGTAGGAATGATGGTTCGAAAAAGTACTGTGGGGAAGATTATGTTCTGAAG 386
QY 490 TCTTGGGTATTCGTTCTTGTGATAGTACAAAGTTAGTCGAGCAAGCTGTTGGAATGCCAT 549
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
387 TCTTGGGTATTCGTTCTTGTGATAGTACAAATAGTCGAGCAAGCTGTTGGAATGCCAT 446
QY 550 CAGTTGGCCCAATATTCAGAGTCCATAGTGAAGCCTTCTTTCGGGATATAGAGTAGTG 609
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
447 CAGTTGGCCCAATATTCAGAGTCCATAGTGAAGCCTTCTTTCGGGATATAGAGTAGTG 506
QY 610 TCTTGAGAGATTGTCCTCCATGCGACGATTAGTTGTTGCCACCGAGGTGTCGTGTTA 669
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507 TCTTGAGAGATTGTCCTCCATGCGACGATTAGTTGTTGCCACCGAGGTGTCGTGTTA 566
QY 670 TCCGACCAATTAACCTGGAGATATAGAAAGGGGCTATCTGTTGGTATAGATGCCCT 729
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567 TCCGACCAAGTTAACTGGGAATATATGAAGAAGGACTATCTGTTGGTATAGATGCCCT 626
QY 730 TGGATGCTCTTCTAGGCGTATTGCTAAAGTGGGAACCTGCCTCTCG 775
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
627 TGGATGCTCTGCTAAGCGTATTGCTAAAGTGGGAACCTGCCTCTCG 672

RESULT 5
B0577650 582 bp mRNA linear EST 19-JUN-2002
LOCUS 3524.1_39.1_F07.Y.1_3524 - Mature pollen from Sheila McCormick's
DEFINITION lab Zea mays cDNA, mRNA sequence.
ACCESSION B0577650
VERSION BQ577650.1 GI:21480967
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 582)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL University
COMMENT Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 725 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3524.1_39.1 row: F column: 07.
FEATURES
source
1..582
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="pollen"
/dev_stages="mature"
/lab_host="SOLR"
/clone_lib="3524 - Mature pollen from Sheila McCormick's

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lab" note="vector: Stratagene's Uni-Zap XR (pBluescript SK-); Site 1: EcoRI (5-prime); Site 2: XhoI (3-prime); Unamplified cDNA library directionally cloned by Rma Kulikaukas using Stratagene's Uni-Zap system. Insert sizes ranged from 0.5kb to 2kb. 50 microliter aliquot had 338,000 pfu when it was made in Sept, 1995, from oligo dt-primed poly A+ RNA."

ORIGIN

Query Match	47.2%	Score 566;	DB 5;	Length 582;
Best Local Similarity	100.0%;	Prod. No. 4.8e-126;		
Matches 566;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCGCGCACCGAGCTACCGTGCCTTCTCTCTCTCTCTTTACACCTACACCTCCGGATCGGCTC	60	
Db	17	CCGCGCACCGAGTACCGTGCCTTCTCTCTCTCTTTACACCTACCTCCGGATCGGCTC	76	
Qy	61	AGAGAGTCAGAGATTCGAGTTGAGCTATAGCGTAGCCGACTGTCGCGGCTCCCTCTCT	120	
Db	77	AGAGAGTCAGAGATTCGAGTTGAGCTATAGCGTAGCCGACTGTCGCGGCTCCCTCTCT	136	
Qy	121	CGGCTCCACCCGCGAGCGACAAATGAGGCGGGGGGGCGTCGGGCTGCGGCTGCAGGGCC	180	
Db	137	CGGCTCCACCCGCGAGCGAAACAATGAGAGCGGGGGGGCGTCGGGCTGCGGCTGCAGGGCC	196	
Qy	181	GGGCGGGGGGCTTCGGGCTCCAGCGGGGCACCGGGGCGGCTTACAGCGCCGCCACCGGGAGCC	240	
Db	197	GGGCGGGGGGCTTCGGGCTCCAGCGGGGCACCGGGGCGGCTTACAGCGCCGCCACCGGGAGCC	256	
Qy	241	TGAGAGTCGCTGACCCCGCGCGGAGCTTCGGGTCGCTGTGCGGGCTCGCGGGTCCAAGCCCG	300	
Db	257	TGAGAGTCGCTGACCCCGCGCGGAGCTTCGGGTCGCTGTGCGGGCTCGCGGGTCCAAGCCCG	316	
Qy	301	TCGCACCGCTCCGAGCTCGTCCGAGAGAAATCGTCCGGAGGTCATGAAACCTCGCACAACT	360	
Db	317	TCGCACCGCTCCGAGCTCGTCCGAGAGAAATCGTCCGGAGGTCATGAAACCTCGCACAACT	376	
Qy	361	CCGTTGACGAAGCTCTCCTGTTGAAGAGAAATCAGAGAAAGTTCTCTGTTCTTACTTTGAACG	420	
Db	377	CCGTTGACGAAGCTCTCCTGTTGAAGAGAAATCAGAGAAAGTTCTCTGTTCTTACTTTGAACG	436	
Qy	421	GGAGGTGTATTACTAGTAGGAATGATGGGTTCTGGNAAAAGTACTGTGGGGGAAGATTA	480	
Db	437	GGAGGTGTATTACTAGTAGGAATGATGGGTTCTGGNAAAAGTACTGTGGGGGAAGATTA	496	
Qy	481	TGCTGAAGTCTGGGTTATTTCGTTCTTTGATAGTGACAACTTAGTGAGCAAGCTGTTG	540	
Db	497	TGCTGAAGTCTGGGTTATTTCGTTCTTTGATAGTGACAACTTAGTGAGCAAGCTGTTG	556	
Qy	541	GAATGCCATCAGTTGCCCAATATTC	566	
Db	557	GAATGCCATCAGTTGCCCAATATTC	582	

RESULT 6

CB684025

LOCUS

DEFINITION

1
2
3
4
5
6
7
8

ACCESSION
NUMBER

VERSION
KEYWORD

KEYWORDS
SOURCE

ORGANIZATIONAL

11

REFERENCE

AUTHOR

TTTTT.E

ENTTY

**JOURNAL
COMMENT**

Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>

```
FOR FRAMES1B
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: C column: 12
Seq primer: gta aaa cga cgg cca gta.
```

FEATURES

Source

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNFI3C12"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNFI"
/notes="vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"

```

ORIGIN

Query Match 47.2%; Score 566; DB 6; Length 825;
Best Local Similarity 84.3%; Pred. No. 5e-126;
Matches 670; Conservative 0; Mismatches 101; Indels 24; Gaps 2;

Qy 149 GCGCGGGGCGTCGGCGCTGGCGCTGCAGGCGCGGGCGCGGGCTTCGCTCGAGCCGGCA 208

Dd 36 GGAGGCGGGCGCTGGGGCTGGCGTGCATCGCGGGCGCGGGGTTTCGGCGGCTCCGACCG 95

Qy 209 CCGG-----GGCGGCTACAGGCGGCCACCGGGAGCCTGAGAGTCGC 250

Db 96 CCGCGGAGCGCGCTCTACGCGCGCAGGGGGCGGGCGCGGATCGGGAGCTTGAGGGTCGC 155

Qy	251	TGACCCGGCGGACCTCGGGTCGCTGTGCGGGCTCGGGGTCAAGCCCGTCGACCGCT	310
Dd	156	TGAGCCGGCGGTGGCAAGGCGCTGTGTGGCTCGCGGGTCAAGCCGGTCGCCCCG	213

Qy	311	CGACTCCGTCGAAGAAATCGTCCGAGGTCATGAAAACTCGACAACCTCCGTTGACGA	370
Db <td>214</td> <td>-----CTCCGTGCCAAGAAATCGTCCGAGGTCATGAAACATTGTCATAACTGGTTGATCA</td> <td>269</td>	214	-----CTCCGTGCCAAGAAATCGTCCGAGGTCATGAAACATTGTCATAACTGGTTGATCA	269

Qy	371	AGCTCTCTCTGTTGAAGAGAAAAATCAGAGAAGTCTCTTCTACTTGAACGGGAGGTGTAT	430
Dh	270	AGCCCTCTTGTCTATACAGAGAAATCAGAGAAGTCTCTTCTTCTTATTTGAATCGACGCTGTAT	328

Qy	431	TTACCTAGTAGGAATGATGGGTTCTGGAAAAAGTACTCTGGGGAAGATTATGTCTCTGAAGT	490
Dh	230	TTTACCTAGTCTGGAATGATGGGTTCTGGAAAAAGTACTCTGGGGAAGATTATGTCTCTCTGAGT	288

[illegible][illegible]

QY 611 CTTGAGAGATTGTCTCCATCGGACGATTAGTTGTGCCACGGAGGTGGTGCCTGTTAT 670

Qy CCGACCAATTAACTGGAGATATGAAGAGGGCCCTATCTGTTTGGTTAGATGTCGCCCTT 730

QY 731 GGATGCTCTTGCTAGCGGTATTGCTAAAGTGGGAAGTCTCGTCTCTTCTGGACCA 790
 |||
 Db 630 GGACGCTCTTGCTAGCGGTATTGCTANAGTGGGACTGCTCCGTCCTTCTTAGATCA 689
 |||
 QY 791 ACCATCTGGTGATCCCTAGCAATGGCCCTTTTCTAAGCTCAGCATGCTTGGCAGCAAAAG 850
 |||
 Db 690 ACCATCTGGTGATCCATACACAAATGGCTTTTCTAAGCTCAGCATGCTCGCGGAGCAAG 749
 |||
 QY 851 GGGTGATGCTTATGCAAAATGCAAGATGAAGGTTTCTCTGGAAGAGATTGCATGTAAACA 910
 |||
 Db 750 GGGCGCATGCTTATGCAAAATGCTGATGTAGGGTTTCTCTTGAAGAGATTGCATCTAAACA 809
 |||
 QY 911 AGGTCAATGATGATGT 925
 |||
 Db 810 GGGTCATGATGATGT 824
 |||

RESULT 7
 COS24949
 LOCUS
 DEFINITION
 3530.1_165.1_C06.Y.1 3530 - Full length cDNA library created by
 Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
 COS24949
 COS24949.1 GI:50329823

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays
 Eukaryota
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 549)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 3530.1.165.1 row: C column: 06.

FEATURES
 source
 1..549
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="multiple"
 /dev_stage="varies by tissue"
 /lab_host="DH10B"
 /clone_lib="3530 - Full length cDNA library created by
 Invitrogen from multiple tissues"
 /note="Organ: silks, husks, ears, pollen, shoot tips,
 leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
 6.1; Site_1: EcoRV; Site_2: NotI; Maize Gene Discovery
 Project contracted with Invitrogen to produce a
 normalized, full length library in a pSport vector. This
 is a Gateway compatible vector, permitting clone movement
 to new vector backbones for expression in diverse host
 cells using recombination rather than restriction enzymes.
 Details of the vector and sequencing primers are available
 at ZmDB in the EST library description tables. poly(A)+
 mRNA was prepared by Invitrogen, and equimolar amounts of
 RNA from each of the 12 tissue samples were mixed together
 for selection of mRNA with a 5' cap. After synthesis of
 cDNA, a normalization step was conducted against the
 mixture of RNA sources. This step effected a 20X to 80X
 reduction in common transcript types. Tissues prepared: 1.
 just emerging silks; 2. inner husks from ears of sample
 #1; 3. 20 dap aleurone; 4. immature tassels, stages from
 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm

ORIGIN

Query Match 45.8%; Score 549; DB 7; Length 549;
 Best Local Similarity 100.0%; Pred. No. 6.2e-122;
 Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 98 CGACTGGTGGCGGCTCCCTCTCGGCTCCACCCGGCGAGCAACAATGGAGGCGGGGG 157
 |||
 Db 1 CGACTGGTGGCGGCTCCCTCTCGGCTCCACCCGGCGAGCAACAATGGAGGCGGGGG 60
 |||
 QY 158 CGTGGGCTTGGCGCTGCAGGGCGGCGGCGGCTTCGGCTCCAGCCCGCACCGGGGGCG 217
 |||
 Db 61 CGTGGGCTTGGCGCTGCAGGGCGGCGGCGGCTTCGGCTCCAGCCCGCACCGGGGGCG 120
 |||
 QY 218 CCTCAGGGGCCACCGGAGGCTGAGAGTGCCTGACCCGGCGGACCTCGGTCGCTGT 277
 |||
 Db 121 CCTCAGGGGCCACCGGAGGCTGAGAGTGCCTGACCCGGCGGACCTCGGTCGCTGT 180
 |||
 QY 278 GCGGCTCGGGTCCAAAGCCGTCGACCCGCTCGACCTCCGTCGGAAGAAATCGTCGG 337
 |||
 Db 181 GCGGCTCGGGTCCAAAGCCGTCGACCCGCTCGACCTCCGTCGGAAGAAATCGTCGG 240
 |||
 QY 338 AGGTGATGAAAACTCGCACAACTCCGTTGACGAAGCTCTCTGTTGAAGAGAAAAATCAGA 397
 |||
 Db 241 AGGTGATGAAAACTCGCACAACTCCGTTGACGAAGCTCTCTGTTGAAGAGAAAAATCAGA 300
 |||
 QY 398 AGAAGTCTGTTCTACTTTGAACGGGAGGTGATTTACCTAGTAGGAATGATGGGTTCTGG 457
 |||
 Db 301 AGAAGTCTGTTCTACTTTGAACGGGAGGTGATTTTACCTAGTAGGAATGATGGGTTCTGG 360
 |||
 QY 458 AAAAGTAGTGTGGGGAAGATTATGCTGAAGCTTTGGTATTTCGTTCTTTGATAGTGA 517
 |||
 Db 361 AAAAGTAGTGTGGGGAAGATTATGCTGAAGCTTTGGTATTTCGTTCTTTTATAGTGA 420
 |||
 QY 518 CAAAGTTAGTGAGCAAGCTGTTTGGAAATGCCATCAGTTGCCAAATATTCAAGGTCATAG 577
 |||
 Db 421 CAAAGTTAGTGAGCAAGCTGTTTGGAAATGCCATCAGTTGCCAAATATTCAAGGTCATAG 480
 |||
 QY 578 TGAAGCCTTTCTTCGGGATAATGAGAGTAGTGCTTTGAGAGATTGTCTCCATGGGAGC 637
 |||
 Db 481 TGAAGCCTTTCTTCGGGATAATGAGAGTAGTGCTTTGAGAGATTGTCTCCATGGGAGC 540
 |||
 QY 638 ATTAGTTGT 646
 |||
 Db 541 ATTAGTTGT 549
 |||

RESULT 8

CA452817/c
 LOCUS
 DEFINITION
 Rp3A-3_H01 subtracted cDNA library of maize inbred line H95-Rp3A
 inoculated with Puccinia sorghi isolate IN1 Zea mays cDNA clone
 Rp3A-3_H01, mRNA sequence.
 CA452817
 CA452817.1 GI:24934599
 EST.
 Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

vegetative shoot tips from 15 day old seedlings; all
 leaves with an expanded or partially expanded sheath
 were removed; 8. mature leaf tissue; 9. 0.5 cm long root
 tips from 15 day old seedlings; 10. 10 dap whole seed; 11.
 12 dap endosperm and embryo; 12. 17 dap endosperm and
 embryo. All of the sequenced clones in project 3530 will
 be archived at the University of Arizona along with the
 Unigene clones from the Maize Gene Discovery EST
 sequencing projects. Clones can be ordered through the
 ZmDB web site or directly from the University of Arizona
 (http://www.genome.arizona.edu/orders/). High density
 filters containing over 18,000 clones can also be ordered
 from the University of Arizona."

clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 619)
Bai, J., Fellers, J.P., Leach, J.E. and Hulbert, S.H.
Comparison of pathogen induced defense gene profiles on maize lines
with different resistance genes
Unpublished (2003)
Contact: Bai J
Department of Plant Pathology
Kansas State University
4024 Throckmorton Plant Sciences Center, Manhattan, KS 66506, USA
Tel: 785-532-2328
Fax: 785-532-5692
Email: jianfa@plantpath.ksu.edu
Seq primer: T7.
Location/Qualifiers
1. .619
/organism="Zea mays"
/mol_type="mRNA"
/strain="inbred line H95-Rp3A"
/db_xref="taxon:4577"
/clone="Rp3A-3 H01"
/tissue_type="Rust-infected leaves"
/dev_stage="4 week-old plants"
/clone_lib="subtracted cDNA library of maize inbred line
H95-Rp3A inoculated with Puccinia sorghi isolate IN1"
/notes="Vector: pUC19; Suppression subtractive
hybridization; cloned into pUC19 vector. From a subtracted
cDNA library of maize inbred line H95 carrying the Rp3A
gene inoculated with an incompatible Puccinia sorghi
isolate."
45.6%; Score 547.8; DB 6; Length 619;
Query Match
Best Local Similarity 93.2%; Pred. No. 1.2e-121;
Matches 573; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
465 ACTGTGGGGAAGATTATGCTGAAGCTTTGGGTTATTGTTCTTTGATAGTACAAAGTTA 524
Db ACTGTGGGGAAGATCATGCTGAAGCTTTGGGTTATTGTTCTTTGATAGTACAAATTA 560
465 GTGAGCAGCTTTGGGATGCCATCAGTTGCCAATATTCAAGTCCATAGTGAAGCC 584
Db GTGAGCAGCTTTGGGATGCCATCAGTTGCCAATATTCAAGTCCATAGTGAAGCC 500
585 TTCTTTCCGGATATGAGAGTAGTGTCTTGAGAGATTGTGCTCCATGCGACGATTAGTT 644
Db TTCTTTCCGGATATGAGAGTAGTGTCTTGAGAGATTGTGCTCCATGCGACGATTAGTT 440
645 GTTGCCACCGAGGTGGTGTCTGTTATCCGACCAATTAAGTGGAGATATATGAAGGGGC 704
Db GTTGCCACCGAGGTGGTGTCTGTTATCCGACCAATTAAGTGGAGATATATGAAGGGGC 380
705 CTATCTGTTTGGTATAGTGCCCTTGGATGCTTCTGTTAGGGGATATGCTAAAGTGGGA 764
Db CTATCTGTTTGGTATAGTGCCCTTGGATGCTTCTGTTAGGGGATATGCTAAAGTGGGA 320
765 ACTGCTCTCGTCTCTTCTGGACCAACCATCTGCTGATCCGACCAATGGCTTTTCT 824
Db ACTGCTCTCGTCTCTTCTGGACCAACCATCTGCTGATCCGACCAATGGCTTTTCT 260
825 AAGCTCAGCATGCTTGCACGAAAGGGGTGATGCTTATGCAAAATGAGATGTAAGGGTT 884
Db AAGCTCAGCATGCTTGCACGAAAGGGGTGATGCTTATGCAAAATGAGATGTAAGGGTT 200
885 TCTCTGAGAGATTTGATGTAACCAAGGTCATGATGATGCTCTTAAGCTGACCTACT 944
Db TCTCTGAGAGATTTGATGTAACCAAGGTCATGATGATGCTCTTAAGCTGATGCTGACT 140
945 GATATTGCAATTCAGTCACTTCAATAGATCGAGCTTGGTCAATCGAGCACACTGCTGAT 1004
Db GATATTGCAATTCAGTCACTTCAATAGATCGAGCTTGGTCAATCGAGCACACTGCTGAT 80
1005 AGTTTCAGTAGCAGCGCAAGCTGAGTGCAGATCCAGAGGATACAGACCTTTGTAGAAC 1064

Db 79 AATCCAGCTAGGCACTCGCAGCTGAGTCACAGATCCAAAGGATACAGACCTTGTAAAT 20
Qy 1065 CTTAATCCCTTTGTT 1079
Db 19 CTTAATCCCTTCTGTT 5
RESULT 9
CB657302
LOCUS
DEFINITION
CB657302
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzoideae; Oryza.
1 (bases 1 to 833)
Jantassuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
JOURNAL
COMMENT
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: I column: 17
Seq primer: gta aaa cga cgg cca gtc.
FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC12117"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice Blasc (C9240-1)"
ORIGIN
Query Match 45.6%; Score 546.6; DB 6; Length 833;
Best Local Similarity 84.1%; Pred. No. 2.5e-121;
Matches 650; Conservative 0; Mismatches 99; Indels 24; Gaps 2;
Qy 149 GCGCGGGGCGCTCGCGCTGCGCTGAGCGCGGGCGGGCTTGGCTCCAGCGGCA 208
Db 67 GGAGCGGGCGTGGGCTGCGCTGAGTCGCGGGCGGGGCTCGGCGGTCCGACCG 126
Qy 209 CCGG-----GGGGCTACAGGGCCCAAGGGAGCTGAGAGTCCG 250
Db 127 CCGCGGAGCGCGCTCTACGGCGGGCGGGGCGGATCGGGAGTTGAGGTCGC 186
Qy 251 TGACCGGGCGGAGCTGCGGCTCGCTGCGGGCTCGCGGTCGAAGCCGCTGCACCGCT 310
Db 187 TGAGCGGGCGGTGGCGAGGCGCTGCTGCGGCTCGGGTCAAGCGGTCGCCCG-- 244
Qy 311 CCGACTCGTGCAGAGAAATCTCGGAGGTGATGAAACTCGCAACATCCGCTTGACGA 370

Db 245 -----CTCCGTGCGCAAGAAATCGTCCGAGGTGATGAAACATTTGCATTAACATCGGTTGATGA 300

Qy 371 AGCTCTCTCTGTTGAAGAGAAAATCAGAAAGATTCTGTTCTACTTCTGAAACGGAGGTGAT 430

Db 301 AGCCCTCTTGTCTAAAGAGAAAATCAGAAAGATTCTTCTATTGTAATGGACGGTGTAT 360

Qy 431 TTACCTAGTAGGAATCATGGGTTCTGGAAGAGTACTGTGGGAAGATTATGCTGAAAGT 490

Db 361 TTACCTAGTTGGAATGATGGGTTCTGGAAGAGTACTGTGGGAAGATTATGCTGAAAGT 420

Qy 491 CTTGGGTTATTCGTTCTTTGATGATGACAGATTAGTGGAGCAAGCTGTTGGAATGCCATC 550

Db 421 TTTGGGTTATTCGTTCTTTGATGATGATAAATTTGGTCGAACAAGCTGTGGGCATGCCCTC 480

Qy 551 AGTTGCCCAAAATATTCAGAGTCCATAGTGAAGCTTCTTTCCGGATAATGAGAGTAGTGT 610

Db 481 AGTCGCTCAAAATTTTCAAGGTTTCATAGTGAAGCTTCTTTTAGGGATAATGAGAGTAGTGT 540

Qy 611 CTTGAGAGATTGTCCTCCATCGACGATTAGTTGTTGTCACCGGAGGTGGTCTGTTAT 670

Db 541 CTTGAGGATTGTCCTCAATGAAGCATTAGTTGTTGCTACTGAGAGGTGGTCTGTTAT 600

Qy 671 CCGACCAATTAACCTGGAGATATATGAAGGGGCCCTATCTGTTGGTTAGATGTGCCCTT 730

Db 601 CCGACCAGTTAACTGGAATACATGAAGAAGGGCCCTATCTGTTGGTTGATGTGCCCTT 660

Qy 731 GGATGCTCTGTAGCGTATGCTTAAAGTGGGAAGTGCCTCTGCTCTCTCTCTCTGACCA 790

Db 661 GGACGCTCTGTAGCGTATGCTTAAAGTGGGAGTGCCTCCCGTCTCTCTCTCTAGATCA 720

Qy 791 ACCATCTGTGTATCGCTGCGCAATGCGCTTTTCTAAGCTCAGATGCTTGTGCAAGCAAG 850

Db 721 ACCATCTGTGTATCGCTGCGCAATGCGCTTTTCTAAGCTCAGATGCTTGTGCAAGCAAG 780

Qy 851 GGGTGATGCTTATGCAAAATGCAAGTAAAGGGTTTCTCTGGAAGAGATTGCAT 903

Db 781 GGGCGATGCTTATGCAAAATGCTGATGCTGAAGGTTTCTCTTGAAGAGATTGCAT 833

RESULT 10

AW671996 609 bp mRNA linear EST 19-JUL-2000

LOCUS LG1.353 All.b1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA

DEFINITION sequence.

ACCESSION AW671996

VERSION EST.

KEYWORDS Sorghum bicolor (sorghum)

SOURCE Sorghum bicolor

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 609)

AUTHORS Cordonnier-Pratt M.-M., Gingle A., Marsala C. and Pratt L.H.

TITLE An EST database from Sorghum: light-grown seedlings

JOURNAL Unpublished (2000)

COMMENT Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV

High quality sequence stop: 607

POLYA=No. Location/Qualifiers

1..609

/organism="Sorghum bicolor"

/mol_type="mRNA"

FEATURES

source

/db_xref="taxon:4558"

/clone_lib="Light Grown 1 (LG1)"

/note="Organ: 10- to 14-day-old light-grown (greenhouse) seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

ORIGIN

Query Match 45.2%; Score 542; DB 2; Length 609;

Best Local Similarity 94.1%; Pred. No. 3.1e-120;

Matches 576; Conservative 0; Mismatches 30; Indels 6; Gaps 1;

Qy 259 CGGACCTTCGGTCTGCGGGCTCGGGTCCAAAGCCGCTCCACCGCTCCGACTCC 318

Db 4 CAGGGCTGCGGTTGCCGTGCGGGTCCAGCCGCTCCACCG-----CTCC 57

Qy 319 GTGCCAAGAAATCGTCCGAGGTCAATGAAACTCGCACAACTCCGTTGACGAAGCTCTCC 378

Db 58 GTGCCAAGAAATCGTTCGAGGTCAATGAAACTTCGATAACTCCGTTGACGAAGCTCTCC 117

Qy 379 TGTGAAAGAAAAATCAGAAAGTTCTGTTCTACTTGAACGGGAGGTGTTATTACCTAG 438

Db 118 TGTGAAAGAAAAATCCGAAGAGTTCTGTTCTACTTGAACGGGAGGTGTTATTACCTAG 177

Qy 439 TAGGAATCATGGTTCGMAAAAGTACTGTGGGGAAGATTATGCTGAAGTCTTGGGTT 498

Db 178 TAGGAATCATGGTTCGMAAAAGTACTGTGGGGAAGATTATGCTGAAGTCTTGGGTT 237

Qy 499 ATTCTCTTCTTTGATGATGACAAAGTTAGTGGAGCAAGCTGTTGGAATGCCATCAGTTGCC 558

Db 238 ATTCTCTTCTTTGACAGTACAAAATTAGTGGAGCAAGCTGTTGGAATGCCATCAGTTGCC 297

Qy 559 AAATATTCAGGTTCATAGTGAAGCCTTCTTTCCGGATAATGAGAGTAGTGTCTTGAGAG 618

Db 298 AAATATTCAGGTTCATAGCAGAAAGCCTTCTTTCCGGATAATGAGAGTAGTGTCTTGAGAG 357

Qy 619 ATTTGCTCTCCATGCGACGATTAGTTGTCACCGGAGGTGGTCTGTTATCCGACCAA 678

Db 358 ATTTGCTCTCCATGCAACGATTAGTTGTCACCGGAGGTGGTCTGTTATCCGACCAA 417

Qy 679 TTAAGTGGAGATATATGAAGGGGCCCTATCTGTTGGTTAGATGTCCTTTGGATGCTC 738

Db 418 TTAAGTGGAAATATATGAAGAGGCCCTATCTGTTGGTTAGATGTCCTTTGGATGCTC 477

Qy 739 TTGCTAGGCGTATTCGTAAGTGGAACTGCTCTCGTCTCTTTGACCAACCATCTCG 798

Db 478 TTGCTAGGCGTATTCGTAAGTGGAACTGCTCTCGTCTCTTTGACCAACCATCTCG 537

Qy 799 GTGATCCGTAGCAATGGCCTTTCTAAGCTCAGCATGCTTGCACAGCAAGGGGTGATG 858

Db 538 GTGATCCATACAAATGGCCTTCTTAAGCTCAGCATGCTTGCACAGCAAGGGGTGATG 597

Qy 859 CTTATGCAAAATG 870

Db 598 CTTATGCAAAATG 609

RESULT 11

CF033002/c

LOCUS QCF11b08.yg QCF Zea mays cDNA clone QCF11b08, mRNA linear EST 17-JUL-2003

DEFINITION CF033002

ACCESSION CF033002

VERSION CF033002.1 GI:32928190

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 620)

AUTHORS Genoplante.

TITLE Genoplante, a major partnership french program in plant genomics

JOURNAL COMMENT	Unpublished (2003) Contact: Genoplatante Genoplatante 93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10 This sequence has been generated in the framework of the french plant genomics programme 'Genoplatante' (http://www.genoplatante.com) and http://genoplatante-info.infobiogen.fr/ .
FEATURES	Location/Qualifiers 1..620 /organism="Zea mays" /mol_type="mRNA" /cultivar="F2" /db_xref="taxon:4577" /clone="OCF11b08" /issue_type="seedling minus kernel" /clone_lib="QCF"
SOURCE	
ORIGIN	Query Match 45.1%; Score 540.8; DB 6; Length 620; Best Local Similarity 92.4%; Pred. No. 6e-120; Matches 569; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY	465 ACTGTGGGGAAGATTATGTCTGAAGTCTTGGGTATTCTTCTTGATAGTGCACAAAGTTA 524
Db	620 ACTGTGGGGAAGTCCATGTCTGAAGTCTTGGGTATTCTTCTTGATAGTGCACAAATTA 561
QY	525 GTGGACAAGCTGTTGGAAATGCATCAGTTCGCAAAATATTCAGGTCCATAGTGAAGCC 584
Db	560 GTGGACAAGCTGTTGGAAATGCCTTCAGTTGCTCAAAATATTCAAAGTTCACAGCAAGCC 501
QY	585 TTCTTTCCGGGATAATGAGAGTAGTGTCTTTGAGAGATTTGCTCTCCATCGCAGCATTAGTT 644
Db	500 TTCTTTCCGGGATAATGAGAGTAGTGTCTTTGAGGATCTCTCTCCATCGCAGCATTAGTT 441
QY	645 GTTGCCACCGAGGTGGTGTGTATTCGACCAATTAATCTGAGAGATATATGAAGAGGGGC 704
Db	440 GTTGCCACCGAGGTGGTGTGTATTCGACCAATTAATCTGAGGATTAATGAAGAGGGGC 381
QY	705 CTATCTGTTTGGTATAGATGTCCTTGGATGCTCTTGTAGGCGTATTCTTAAGTGGGA 764
Db	380 CTATCTGTTTGGTATAGATGTCCTTGGATGCTCTTGTAGGCGTATTCTTAAGTGGGA 321
QY	765 ACTGCTCTCGTCTCTTCTGGACCAACCATCTGTGTGATCCGTAGCAGCATGSCCTTTTCT 824
Db	320 ACGGCTTCTCGTCTCTTCTGGACCAACCGTCGGGTGATCCATACAAATGSCCTTTTCT 261
QY	825 AAGCTCAGCATGTTGCAAGCAAGGGGTGATGCTTATGCAAAATGCAGATGTAAGGGTT 884
Db	260 AAGCTCAGCATGTTGCAAGCAAGGGGTGATGCTTATGCAAAATGCGGATGTAAGGGTT 201
QY	885 TCTCTGGAAGATTCATGTAACCAAGCTCATGATGTCTCTTAAGCTGCACCTACT 944
Db	200 TCTCTGGAAGATTCATGTAACCAAGCTCATGATGTCTCTTAAGCTGCACCTACT 141
QY	945 GATATTGCAATTGAGTCACTTCATAGATCGAGAGCTTCGTTCATCGAGCACACTGCTGAT 1004
Db	140 GATATCGCAATTGAGTCACTTCATAGATCGAGAGCTTCGTTCATCGAGCACCTGCTGAT 81
QY	1005 AGTTACGTAGGACCGCGCAAGCTGATGTCGAGATCCAGAGGATCAGACCTTTAGAAC 1064
Db	80 AATCCAGCTAGGACCTCGCAAGCTGATGTCAGATCCAAAGGATACAGACCTTTGAATAT 21
QY	1065 CTTAATCCCTTTGTTT 1080
Db	20 CTTAATCCCTTTGTTT 5
RESULT 12	
CF636791/c	
LOCUS	CF636791 814 bp mRNA linear EST 02-OCT-2003
DEFINITION	zmrw00_0B10-012-g04.s3 zmrw00 Zea mays cDNA 3', mRNA sequence.

ACCESSION	CF636791
VERSION	CF636791.1
KEYWORDS	GI:37398941
SOURCE	EST.
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 814) Bohnert,H., Sharp,R.E., Springer,G.K., Poroyko,V., Fredricksen,M., Sharp,L.G., Spollen,W.G., Ries,J., Guillen,A., Khambati,A., Topinka,C., Davis,G.E., Schachtman,D., Wu,Y. and Nguyen,H.T.
TITLE	NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root Signaling Under Drought
JOURNAL	Unpublished (2003)
COMMENT	Contact: Hans Bohnert University of Illinois, Urbana-Champaign 1201 West Gregory Drive, Urbana, IL 61801, USA Tel: 217-265-5475 Fax: 217-333-5574 Email: bohnert@life.uiuc.edu POLYA=Yes.
FEATURES	Location/Qualifiers 1..814 /organism="Zea mays" /mol_type="mRNA" /db_xref="taxon:4577" /clone_lib="zmrw00" /note="Samples were collected in Robert E. Sharp's lab (University of Missouri-Columbia) to construct three normalized cDNA libraries. Dark-grown maize seedlings with primary roots 12-20 mm in length were transplanted to high (-0.03 MPa) or low water potential (-1.6 MPa) vermiculite, and harvested at 5 h and 48 h after transplanting. About 1,000 roots were used for each of the low water potential libraries (zmrw05 and zmrw48) while 500 roots were combined from each of the two time points at high water potential (zmrw00). Each root was divided into 4 segments (distances are from the junction of the root apex and root cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7 mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details of conditions see (1) with nutrient modifications as in (2)). The three normalized cDNA libraries were constructed in the lab of Hans Bohnert (University of Illinois-UC). Total RNA was extracted by the 'hot phenol' method (Plant Molecular Biology manual, D5: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)+mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)+mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (root_segment1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of s0 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adaptor with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E.coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw05: 3.37 x 10 ⁶ ; zmrw48: 4.87 x 10 ⁶ ; zmrw00: 3 x 10 ⁶ . The background of empty clones was less than 1%. Inserts ranged from -0.5Kb to >2.5 kb, as determined by

PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 30°C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electrophoreted into DH10B. The total number of clones with insert was: zmrws05: 2.0x10⁷; zmrws48: 4.2x10⁷; zmrws00: 1.1x10⁷. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5kb to 2.5kb. (1) Sharp R E; Silk W K; Heiao T C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50-57. (2) Spollen W G; LeNoble M E; Samuels T D; Bernstein N; Sharp R E. Abscissic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122(3). March, 2000. 967-976.
TAG_TISSUE=Root_segment_3
TAG_SEQ=TCGCA"

ORIGIN

Query Match 44.8%; Score 537.2; DB 7; Length 814;
Best Local Similarity 92.2%; Pred. No. 4.6e-119;
Matches 566; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 472 GGAGATTATGCTGAAGTCTGGGTATTCGTTCTTCATAGTACAGATTAGTGGAGC 531
DB 806 GGGAGATCATGCTGAAGTCTGGGTATTCGTTCTTCATAGTACAAATTAGTGGAGC 747

QY 532 AAGCTCTTGGATGCGCATCAGTTGCCAAATATTCAGGTCCATAGTGAAGCTCTCTTTC 591
DB 746 AAGCTCTTGGATGCGCATCAGTTGCTCAATATTCAGGTTCACAGGAGCTCTTTC 687

QY 592 GGGATTAATGAGAGTATGCTCTTGAGAGATTGTTCTCCATGCGACGATTAGTTGGCA 651
DB 686 GGGATTAATGAGAGTATGCTCTTGAGAGATTGTTCTCCATGCGACGATTAGTTGGCA 627

QY 652 CCGGAGTGGTCTGTTATCCGACCAATTAACGTGGAGATATAGAGAGGCGCTATCTG 711
DB 626 CCGGAGTGGTCTGTTATCCGACCAATTAACGTGGAGATATATGAAGAAGGCGCTATCG 567

QY 712 TTTGGTTAGATGTCCTTGGATGCTCTTGGCTAGGCGTATTGCTAAAGTGGGAATGCTCT 771
DB 566 TTTGGTTAGATGTCCTTGGATGCTCTTGGCTAGGCGTATTGCTAAAGTGGGAATGCTCT 507

QY 772 CTGCTCCTCTTTGGACCAACCATCTGGTGATCCGTTACGCAATGGCCTTTTCTAAGCTCA 831
DB 506 CTGCTCCTCTTTGGACCAACCATCTGGTGATCCGTTACGCAATGGCCTTTTCTAAGCTCA 447

QY 832 GCATGCTTCCAGCAAGGCGGTGATGCTTATGCAATGCAGATGTAAGGTTCTCTCG 891
DB 446 GCATGCTTCCAGCAAGGCGGTGATGCTTATGCAATGCAGATGTAAGGTTCTCTCG 387

QY 892 AAGAGATTGCATGTAACCAAGGTTCATGATGATGCTCTTAAGCTGCACCTACTGTGATATTG 951
DB 386 AAGAGATTGCATGTAACCAAGGTTCATGATGATGCTCTTAAGCTGCACCTACTGTGATATTG 327

QY 952 CAATTGAGTCACTTCATATAAGATCAGAGTTCGTTCATCGAGCACACTGCTGATAGTTTCAG 1011
DB 326 CAATTGAGTCACTTCATATAAGATCAGAGTTCGTTCATCGAGCACACTGCTGATAGTTTCAG 267

QY 1012 CTAGCCAGCGCAAGCTGAGTGCAGATCCAGAGGATACAGACCTTGTAGACCTTAATC 1071
DB 266 CTAGCCAGCTGCAAGCTGAGTGCAGATCCAGAGGATACAGACCTTGTAGACCTTAATC 207

QY 1072 CCTTTTGTGGCCAC 1085
DB 1072 CCTTTTGTGGCCAC 1085

DB 206 CTTCTGTTTTGTAC 193

RESULT 13
CA105686
LOCUS
DEFINITION
SCJFHRIC08D05.g HR1 Saccharum officinarum cDNA clone SCJFHRIC08D05
5', mRNA sequence.
CA105686 650 bp mRNA linear EST 23-SEP-2003
SCJFHRIC08D05

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.

REFERENCE
1 (bases 1 to 650)
Vettore, A.L., da Silva, P.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: C08 Row: D Column: 05
Seq primer: 17 Promoter Primer.
Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="HR1"
/note="Organ: seedlings inoculated with Herbaspirillum
rubrisubalbicans; Vector: pSport1; Site 1: SalI; Site 2:
NotI; An unidirectional cDNA library generated from
rubrisubalbicans; cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 44.2%; Score 530.8; DB 6; Length 650;
Best Local Similarity 93.0%; Pred. No. 1.6e-117;
Matches 569; Conservative 0; Mismatches 37; Indels 6; Gaps 1;

QY 130 CCGCGCAGCGAACAAATGGAGCGGGGCGTGGCTCGCGTGCAGCGGGCGGGCGG 189
DB 45 CCGCGCAGCGAACAAATGGAGCGGGGCGTGGCTCGCGTGCAGCGGGCGGGCGG 104

QY 190 GCTTCGGTCCAGCGGCACCGGGCGGCTACAGCGCCACCGGAGCCTGAGAGTCG 249
DB 105 GCTTCGGTCCAGCGGCACCGGGCGGCTACAGTCGCCCGGAGCCTCAGAGTCG 164

QY 250 CTGACCCCGCGGACCTCGGTCGCTGTGCGGCTCGGGGTCCAAAGCCGTCGACCCG 309
DB 165 CTGACCCCGCGGAGCAGCGGTGCTGTGCGGCTCGGGGTCCAAAGCCGTCGACCCG- 223

QY 310 TCCGACTCCGTCGGAAGAAATCGTCCGAGGTCATGAAACAACTCGCACAACTCGTTGACG 369
DB 224 -----CTCCGTGCGAAGAAATCGTTCCGTTGGTTCATGAAACCTTGATTAACCTCGTTGACG 278

LOCUS CB684026 818 bp mRNA linear EST 09-APR-2003
DEFINITION OSJNEF13C12_r OSJNEF Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEF13C12 3', mRNA sequence.

ACCESSION CB684026
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 818)

AUTHORS Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

TITLE Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea

JOURNAL Unpublished (2003)

COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

PCR Primers
FORWARD: gta aaa cga cgg cca gtcg
BACKWARD: gga aac agc tat gac cat g

Plate: 13 row: C column: 12
Seq primer: gga aac agc tat gac cat g.

FEATURES
Location/Qualifiers
1..818

/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nipponbare"
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/clone="OSJNEF13C12"
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/dev_stage="3 week"
/lab_host="DH10B"

/clone_lib="OSJNEF"
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XhoI; Uninfected Control"

ORIGIN

Query Match 43.4%; Score 520.8; DB 6; Length 818;
Best Local Similarity 79.7%; Pred. No. 4.3e-115;
Matches 630; Conservative 0; Mismatches 152; Indels 8; Gaps 1;

417 AACGGAGGTGATTTTACCTAGTAGGAATGATGGGTTCTGGAAAAAGTACTGTGGGAAG 476
418 AATGGACGGTGTATTTACCTAGTTGGAAATGATGGGTTCTGGAAAAAGTACTGTGGGAAG 759

477 ATTATCTCTGAAGTCTTGGGTTATTCTGTTCTTTTGATAGTGACAAAGTTAGTGGAGCAAGCT 536
478 ATCATGTCGAAGCTTTGGGTTATTCTGTTCTTTTGATAGTATAAATTTGGTCGAACAAGCT 699

537 GTTGGAAATGCCATCAGTTCGCCAAATATTCAGGTCATAGTGAAGCCTTCTTCGGGAT 596
538 GTGGGATGCTCTTCAAGTTCGCTCAAAATTTTCAAGGTTTCATAGTGAAGCCTTCTTCGGGAT 639

597 AATGACAGTAGTCTTTGAGAGATTGTCTCCATCGACGATTTAGTTGTCACCGGA 656
598 AATGACAGTAGTCTTTGAGAGATTGTCTCCATCGACGATTTAGTTGTCACCGGA 656

638 AATGACAGTAGTCTTTGAGAGATTGTCTCCATCGACGATTTAGTTGTCACCGGA 579
639 AATGACAGTAGTCTTTGAGAGATTGTCTCCATCGACGATTTAGTTGTCACCGGA 579

657 GGTGGTCTGCTTTATCCGACCAATTAATGGAGATATATGAAGAGGGGCCCTATCTGTTGG 716
658 GGTGGTCTGCTTTATCCGACCAATTAATGGAGATATATGAAGAGGGGCCCTATCTGTTGG 519

717 TTAGATGTCCTTGGATGCTTCTGCTAGCGTATTGCTAAAGTGGGAAGTCTGCTCTCGT 776
718 TTGATGTCCTTGGATGCTTCTGCTAGCGTATTGCTAAAGTGGGAAGTCTGCTCTCGT 459

777 CCTCTTTGGACCAACCATCTGGTGATCCGTACGCAATGGCCTTTCTAAAGCTCAGCATG 836
458 CCTCTTTTAGATCAACCATCTGGTGATCCATACACAATGGCTTTTCTAAGCTCAGCATG 399
837 CTTGCACAGCAAAAGGGGTGATGCTTTATGCAAAATGCAGATGTAAGGGTTTCTCTGGAAGAG 896
398 CTCGCGGAGCAAAAGGGGGGATGCTTTATGCAAAATGCTGATGTGAGGGTTTCTCTGGAAGAG 339
897 ATTGCATGTAACAAGGTTCATGATGCTCTTAAGCTGACACCTCCTGATATTCGAATT 956
338 ATTGCATGTAACAAGGTTCATGATGCTCTTAAGCTGACACCTCCTGATATTCGAATT 279
957 GAGTCACCTTCATAAGATCGAGAGCTTCGTCATCGAGCACACTGCTGATAGTTTCAGCTAGC 1016
278 GAGTCGTTTCATAAGATCGAGAGCTTCGTCATCGAGCACACTGCTGATAGTTTCAGCTAGC 219
1017 GACGCGCAAGCTGAGTCCGAGATCCAGAGGATACAGAGCTTGTGAGAACTTAACTCCCTTT 1076
218 GACTCCAGGCTGACTCAGCTCAGAGGATACAGAGCTTGTGAGAACTTAACTCCCTTT 159
1077 GTTTGC-----CACATAGAGCATCGTTCGCTGAGTTATTGTTAAAGGAATGGAAGAGGA 1128
158 TGTACCTTAGTGTACCTTGTAGCGCTGTTGAGTTATTGTTGCTGTACCCGACAGATG 99
1129 GCTAATAATCCGAAAGTGTGCGCTTGGCTGAAAAAAGGAGGATTTTCTCTGTAAGAAAGGATATATGAGGT 39
98 ATGAAAAAGAACCGGAAGTGTATTTCCTTGTAAACTGTAAAGAAAGGATATATGAGGT 39
1189 AAAAAA 1198
38 AATCAGAAAA 29

Search completed: August 25, 2005, 20:22:24
Job time : 4431 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2005, 10:51:49 ; Search time 167 Seconds
(without alignments)
706.359 Million cell updates/sec

Title: US-10-660-226-10

Perfect score: 1526

Sequence: 1 MEAGGVGLALQARAAGFGSS.....ADSSASDAQESQIQRIQL 305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	656	43.0	303	3	AAG12963		Aag12963 Arabidops
3	650	42.6	220	3	AAG50002		Aag50002 Arabidops
4	650	42.6	220	3	AAG50011		Aag50011 Arabidops
5	650	42.6	220	3	AAG50001		Aag50001 Arabidops
6	650	42.6	250	3	AAG50010		Aag50010 Arabidops
7	649.5	42.6	292	5	ABB91833		Abb91833 Herbicida
8	603	39.5	199	3	AAG49994		Aag49994 Arabidops
9	603	39.5	199	3	AAG50003		Aag50003 Arabidops
10	603	39.5	199	3	AAG50012		Aag50012 Arabidops
11	602	39.4	301	3	AAG42178		Aag42178 Arabidops
12	602	39.4	316	3	AAG42177		Aag42177 Arabidops
13	599	39.3	199	3	AAG12964		Aag12964 Arabidops
14	581	38.1	194	3	AAG49995		Aag49995 Arabidops
15	577	37.8	194	3	AAG12965		Aag12965 Arabidops
16	545	35.7	200	3	AAG42179		Aag42179 Arabidops
17	530.5	34.8	231	3	AAG27626		Aag27626 Arabidops
18	523	34.3	195	3	AAG27627		Aag27627 Arabidops
19	518	33.9	194	3	AAG14899		Aag14899 Arabidops
20	461	30.2	183	3	AAG14899		Aag14899 Arabidops
21	451	29.6	163	3	AAG23896		Aag23896 Arabidops
22	429	28.1	305	5	ABB93307		Abb93307 Herbicida
23	401	26.3	164	3	AAG14900		Aag14900 Arabidops
24	374	24.5	103	5	ABP35328		Abp35328 Human kin
25	350.5	23.0	133	3	AAG14901		Aag14901 Arabidops

26	318.5	20.9	189	8	ADN19967	Adn19967 Bacterial
27	316.5	20.7	188	8	ADS30920	Ads30920 Bacterial
28	311.5	20.4	274	5	ABB92451	Abb92451 Herbicida
29	307	20.1	176	8	ADS42564	Ads42564 Bacterial
30	297	19.5	111	3	AAG23897	Aag23897 Arabidops
31	294.5	19.3	134	8	ADS30077	Ads30077 Bacterial
32	252	16.5	194	8	ADS42142	Ads42142 Bacterial
33	249.5	16.3	168	8	ADN17512	Adn17512 Bacterial
34	243.5	16.0	231	8	ADL04401	Adl04401 M. catarr
35	237.5	15.6	492	8	ADN20281	Adn20281 Bacterial
36	237	15.5	225	7	ABM73793	Abm73793 DNA clone
37	234.5	15.4	200	8	ADS27980	Ads27980 Bacterial
38	231	15.1	180	8	ADR31461	Adr31461 Shikimate
39	228.5	15.0	168	8	ADN25346	Adn25346 Bacterial
40	227.5	14.9	165	8	ADN26123	Adn26123 Bacterial
41	222.5	14.6	166	8	ADN27066	Adn27066 Bacterial
42	222	14.5	200	6	ADA34862	Ada34862 Acinetoba
43	222	14.5	200	7	ABO64295	Abos64295 Klebsiell
44	220	14.4	146	8	ADS43278	Ads43278 Bacterial
45	220	14.4	148	8	ADS28767	Ads28767 Bacterial

ALIGNMENTS

RESULT 1
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ID AAG49993 standard; protein; 303 AA.
XX AC AAG49993;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 63306.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX FN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
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PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
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PR 20-JUL-1999; 99US-0144632P.
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PR 21-JUL-1999; 99US-0145086P.
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PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
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KW	hybridisation assay; genetic mapping; gene expression control; promoter;				
KW	termination sequence.				
XX	Arabidopsis thaliana.				
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Query Match 42.6%; Score 650; DB 3; Length 220;		
Best Local Similarity 62.7%; Pred. No. 1.9e-59;		
Matches 126; Conservative 35; Mismatches 40; Indels 0; Gaps 0;		
QY	81	KEKSEVLFLNGRCIYLVGMWGSGKSTVGKIMSEVLGVSYFFDSKLVQAVGMPSVAOI 140
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QY	141	FKVHSEAFPRDNESVLRDLSSMRLLVWATGGGAVIRPINRMRYMKRGLSVWLDVPLDALA 200
Db	67	FVHGHENFERGKETDALKKLSRYQVWVSTGGGAVIRPINMKYMHKGISILWDVPLEALA 126
QY	201	RIIAKVGTRASRPLDQPSGDPYAMAFSKLSMLAQOQGDYANADVRSLEEIACKQGHDD 260
Db	127	HRIAAGTDSRPLLDHDESGDAYSVAFKRLSAIWDERGEAYTNANARVSLNIAAKRGYKN 186
QY	261	VSKLTPTDIAIESLHKIESFV 281
Db	187	VSDLTPTETAIETAEFEQVLSFL 207
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AAG50001		
ID	AAG50001	standard; protein; 250 AA.
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AC	AAG50001;	
XX		
DT	18-OCT-2000	(first entry)
XX		
DE	Arabidopsis thaliana	protein fragment SEQ ID NO: 63317.
XX		
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
XX		
OS	Arabidopsis thaliana.	
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PN	EP1033405-A2.	
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Best Local Similarity	62.7%;	Pred. No. 2.3e-59;		
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Db	37	QRKAEEVKPYLNGRMYLVGMGSGKTTVGKLSKVLGTFDFCDTLIEQANNGTSVAEI	96	
QY	141	FKVHSAEAFRDNESSVLRDLSSNRRLVATGGGAVIRPINWRYMKRGLSVWLDVPLDALA	200	
Db	97	FVHNGENFFRGKETDALKKLSSRYQVWSTGGGAVIRPINWRYMKRGLSVWLDVPLEALA	156	
QY	201	RRIAKVGTAARPLLDQSGDPYAMAFSKLSMLAQQRDAYANADVRSLEEIACKQGHDD	260	
Db	157	HRIAAGTDSRPLLDHSDGDAVSAPFKRLSAIWDERGEAYTNANARVSLNIAAKRGYKN	216	
QY	261	VSKLTPTDIAIESLHKIESFV	281	
Db	217	VSDLTPTDIAIEAFEQVLSFL	237	
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XX	KW	Protein identification; signal transduction pathway; metabolic pathway;		
XX	KW	hybridisation assay; Genetic mapping; gene expression control; promoter;		
XX	KW	termination sequence.		
XX	OS	Arabidopsis thaliana.		
XX	PN	EP1033405-A2.		
XX	PD	06-SEP-2000.		
XX	PF	25-FEB-2000; 2000EP-00301439.		
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PR 23-AUG-1999;	99US-0149930P.	XX DE Herbicidal; plant; agriculture; herbicide.	
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PR 04-OCT-1999;	99US-0157117P.		

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XX 28-AUG-2001; 2001WO-EP009892.
XX
PA (FARB ) BAYER AG.
PI Tietjen K, Weidler M;
XX
XX WPI; 2002-269010/31.
DR
XX
XX Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms.
XX
XX Claim 5; SEQ ID NO 1044; 261pp + Sequence Listing; English.
XX
XX The invention relates to identifying target proteins (ABB90790-ABB94016)
CC for herbicidally active compounds, comprising aligning and comparing
CC nucleic acid or amino acid sequences from plant with nucleic acid or
CC amino acid sequences from non-plant organisms using suitable search
CC parameters, where plant sequences having an E-value greater by a factor
CC of 3 than the E-value of most similar non-plant sequences are selected.
CC The polypeptides or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as
CC herbicides
XX
XX Sequence 292 AA;
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Best Local Similarity 62.1%; Pred. No. 3.3e-59;
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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ID AAG50003 standard; protein; 199 AA.

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XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 63319.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

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PR 04-AUG-1999;	99US-0147204P.	PR 28-OCT-1999;	99US-0161993P.
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PR 05-AUG-1999;	99US-0147192P.	Query Match 39.5%; Score 603; DB 3; Length 199;	
PR 05-AUG-1999;	99US-0147260P.	Best Local Similarity 62.4%; Pred. No. 1.4e-54;	
PR 06-AUG-1999;	99US-0147303P.	Matches 116; Conservative 33; Mismatches 37; Indels 0; Gaps 0;	
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PR 10-AUG-1999;	99US-0148171P.	1 MYLVGMGSGKTTVGKLSKVLGYTFFDCDTLIEQAMNGTSVAEIFVHHGENFFRGKETD	60
PR 11-AUG-1999;	99US-0148319P.	QY 156 VLRLSSNRRLVWATGGGAVIRPINRWYMKRGLSVWLDPDLALARRIAKYCTASRPILD	215
PR 12-AUG-1999;	99US-0148341P.	Db : : : : : : : : : : :	
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PR 16-AUG-1999;	99US-0149368P.	QY 216 QPSGDPYAMAFSKLSMLAQORGDAYANADVRVSLSEETACKQCHDDVSKLTPTDIAIESLH	275
PR 17-AUG-1999;	99US-0149175P.	Db : : : : : : : : : :	
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PR 27-AUG-1999;	99US-0150666P.	XX AAG42178;	
PR 27-AUG-1999;	99US-0151066P.	AC AAG42178;	
PR 27-AUG-1999;	99US-0151080P.	XX 18-OCT-2000 (first entry)	
PR 30-AUG-1999;	99US-0151303P.	DT XX	
PR 31-AUG-1999;	99US-0151438P.		
PR 01-SEP-1999;	99US-0151930P.		
PR 07-SEP-1999;	99US-0152363P.		
PR 10-SEP-1999;	99US-0153070P.		

DE Arabidopsis thaliana protein fragment SEQ ID NO: 52568.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
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PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
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PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
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PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161922P.
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PR	29-OCT-1999;	99US-0162142P.

Query Match 39.4%; Score 602; DB 3; Length 301;
Best Local Similarity 54.9%; Pred. No. 3.4e-54;
Matches 129; Conservative 38; Mismatches 58; Indels 10; Gaps 5;

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QY	109	VGKIMSEVLGYSPFDSKLVQAVGMPVSAQIFKVHSEAFFRDNESVLRDLSSM-RLV 167
Db	115	VGKIMARSLGYTFPDCDTLIEQAMKGTVAEIFHFGESVREKETEALKKLSMYHQV 174
QY	168	VATGGGAVIRPINWYMKRGLSVWLDVPLDALARRIAKVGTASRPLL-DQPSGDPYAMAF 226
Db	175	VSTGGGAVIRPINWYMKRGLSVWLDVPLDALARRIAKVGTASRPLLHDDESGDTYTAAL 234
QY	227	SKLSMLAQQRDAYANADVRSLEETACKQGHDDVSKLTPTDTAIESLHKIESFV 281
Db	235	NRLSTIWDARGEAYTKASARVSLNITLKLGYRSVSDLTPAETAEAFQVQSYL 289

RESULT 12
AAG42177
ID AAG42177 standard; protein; 316 AA.

XX	AAG42177;	
AC	18-OCT-2000 (first entry)	
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 52567.	
DT	Protein identification; signal transduction pathway; metabolic pathway;	
XX	hybridisation assay; genetic mapping; gene expression control; promoter;	
DE	termination sequence.	
XX	Arabidopsis thaliana.	
KW	EP1033405-A2.	
KW	06-SEP-2000.	
XX	25-FEB-2000; 2000EP-00301439.	
OS	25-FEB-1999; 99US-0121825P.	
XX	09-MAR-1999; 99US-0123180P.	
PR	05-MAR-1999; 99US-0123548P.	
PR	23-MAR-1999; 99US-0125788P.	
PR	25-MAR-1999; 99US-0126264P.	
PR	29-MAR-1999; 99US-0126785P.	
PR	01-APR-1999; 99US-0127462P.	
PR	06-APR-1999; 99US-0128234P.	
PR	08-APR-1999; 99US-0128714P.	
PR	16-APR-1999; 99US-0129845P.	
PR	19-APR-1999; 99US-0130077P.	
PR	21-APR-1999; 99US-0130449P.	
PR	23-APR-1999; 99US-0130510P.	
PR	28-APR-1999; 99US-0130891P.	
PR	30-APR-1999; 99US-0131449P.	
PR	30-APR-1999; 99US-0132048P.	
PR	30-APR-1999; 99US-0132407P.	
PR	04-MAY-1999; 99US-0132484P.	
PR	05-MAY-1999; 99US-0132485P.	
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PR	21-MAY-1999; 99US-0135353P.	
PR	24-MAY-1999; 99US-0135629P.	
PR	25-MAY-1999; 99US-0136021P.	
PR	27-MAY-1999; 99US-0136392P.	
PR	28-MAY-1999; 99US-0136782P.	
PR	01-JUN-1999; 99US-0137222P.	
PR	03-JUN-1999; 99US-0137528P.	
PR	04-JUN-1999; 99US-0137502P.	
PR	07-JUN-1999; 99US-0137724P.	
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PR	10-JUN-1999; 99US-0138540P.	
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PR	14-JUN-1999; 99US-0139119P.	
PR	16-JUN-1999; 99US-0139452P.	
PR	16-JUN-1999; 99US-0139453P.	
PR	17-JUN-1999; 99US-0139492P.	
PR	18-JUN-1999; 99US-0139454P.	
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PR	18-JUN-1999; 99US-0139456P.	
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PR	18-JUN-1999; 99US-0139459P.	
PR	18-JUN-1999; 99US-0139460P.	
PR	18-JUN-1999; 99US-0139461P.	

RESULT 13
AAG12964
ID AAG12964 standard; protein; 199 AA.
XX
AC AAG12964;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12280.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD
XX
PF 06-SEP-2000.
XX
PP 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
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PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134218P.
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PR 20-MAY-1999; 99US-0135124P.
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PR 24-MAY-1999; 99US-0135629P.
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PR 18-JUN-1999; 99US-0139462P.
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PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144353P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.

[illegible]

Query Match 37.8%; Score 577; DB 3; Length 194;
Best Local Similarity 61.3%; Pred. No. 7.5e-52;
Matches 11; Conservative 32; Mismatches 38; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2005, 10:58:14 ; Search time 22 seconds
(without alignments)
1034.907 Million cell updates/sec

Title: US-10-660-226-10
Perfect score: 1526
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PTUS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	222	14.5	200	4	US-09-328-352-6149
3	222	14.5	200	4	US-09-489-039A-10812
4	212.5	13.9	191	4	US-09-543-681A-6682
5	205.5	13.5	184	4	US-09-252-991A-32964
6	185.5	12.2	178	4	US-09-107-532A-5800
7	179	11.7	158	4	US-09-583-110-3547
8	179	11.7	159	4	US-09-107-433-3398
9	167.5	11.0	170	4	US-09-134-000C-4979
10	162	10.6	177	4	US-09-543-681A-5313
11	145	9.5	213	4	US-09-489-039A-13538
12	143.5	9.4	184	4	US-09-198-452A-1113
13	143.5	9.4	184	4	US-09-438-185A-1039
14	140.5	9.2	172	3	US-09-134-001C-3610
15	125	8.2	276	4	US-09-248-796A-18195
16	125	8.2	1551	3	US-09-425-665-2
17	125	8.2	1551	3	US-09-685-668-2
18	103	6.7	1049	4	US-08-727-308-1
19	100	6.6	789	3	US-09-252-991A-25336
20	97	6.4	515	4	US-09-902-540-14617
21	96	6.3	467	4	US-09-252-991A-28862
22	95.5	6.3	353	4	US-09-252-991A-26103
23	95	6.2	2259	3	US-09-413-814-70
24	95	6.2	2439	3	US-09-335-409-7
25	95	6.2	2439	3	US-09-568-102-7
26	95	6.2	2439	3	US-09-567-969-7
27	95	6.2	2439	3	US-09-568-480-7

28	95	6.2	2439	3	US-09-568-486-7	Sequence 7, Appli
29	95	6.2	2439	3	US-09-568-472-7	Sequence 7, Appli
30	95	6.2	2439	3	US-09-567-899-7	Sequence 7, Appli
31	94	6.2	698	4	US-09-828-062-9	Sequence 9, Appli
32	94	6.2	1832	3	US-09-335-403-4	Sequence 4, Appli
33	94	6.2	1832	3	US-09-568-102-4	Sequence 4, Appli
34	94	6.2	1832	3	US-09-567-969-4	Sequence 4, Appli
35	94	6.2	1832	3	US-09-568-480-4	Sequence 4, Appli
36	94	6.2	1832	3	US-09-568-486-4	Sequence 4, Appli
37	94	6.2	1832	3	US-09-568-472-4	Sequence 4, Appli
38	94	6.2	1832	3	US-09-567-893-4	Sequence 4, Appli
39	93.5	6.1	171	4	US-09-328-352-8227	Sequence 8227, Ap
40	93.5	6.1	616	4	US-09-949-016-6889	Sequence 6889, Ap
41	93.5	6.1	616	4	US-09-949-016-7740	Sequence 7740, Ap
42	93	6.1	1413	4	US-09-252-991A-23627	Sequence 23627, A
43	92.5	6.1	549	4	US-09-902-540-10128	Sequence 10128, A
44	92.5	6.1	947	2	US-08-500-857A-4	Sequence 4, Appli
45	92	6.0	209	2	US-08-793-229-29	Sequence 29, Appli

ALIGNMENTS

RESULT 1
US-09-540-236-2087
; Sequence 2087, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2087
; LENGTH: 231
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2087

Query Match 16.0%; Score 243.5; DB 4; Length 231;
Best Local Similarity 30.9%; Pred. No. 1.3e-17;
Matches 69; Conservative 44; Mismatches 75; Indels 35; Gaps 8;

QY 85 BEVLVFLNGR-----CIVLVGMVSGKSTVGKIMSEVLGYSFFDSKLVQAVGMPVS 137
DB 30 ESWVVEKAGNALSKOLPAIFLVGPNAGKTTIGLLAKHLGRNFIDCDWYIYDQTG-ADI 88
QY 138 AQIFKVHSEAFPRDNSESVLRDLSSMRLLVATGGVIRPINWRYMKRGLSVWLDVPLD 197
DB 89 PWIFEKEEGEGRDRETRALQELTALPMIATGGAVGRTKRELLKGLVIYLDASVD 148
QY 198 ALARIKAVGTASRPLLPQSGDPYAMAFSKLSMLAQQRGDAYANADVRSLEEIAKQG 257
DB 149 TQLARTKK--DKNRPLLQ--AQNPRAV---LESYKKRHPLY-----REVA---- 187
QY 258 HDDVSKLT----PTDIAIESLHKIESFVIEHTADSSASDAQAE 296
DB 188 --DIILLTGRAYPKOMIGEILEVLENYALDHAPNKLKTDQHA 228

RESULT 2
US-09-328-352-6149
; Sequence 6149, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04


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US-09-107-532A-5800
; Sequence 5800, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5800:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...178
; SEQUENCE DESCRIPTION: SEQ ID NO: 5800:
US-09-107-532A-5800

Query Match          12.2%   Score 185.5; DB 4; Length 178;
Best Local Similarity 37.08; Pred No. 1.3e-11;
Matches 44; Conservative 29; Mismatches 43; Indels 3; Gaps 3;

QY    96 IYLVMGMSGKSTVGKIMSEVLGYSPFDSDKLVEQAVGMPSVAQIFKVHSEAFRRNESS 155
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB    13 ILLIGFMGACKTTTGKLAQCLOQEYVDLTKTEEHQL-SIAEYPHYXGKSFRKVESD 71

QY    156 VLRLDSMRRLVATGGGAVIRPINWRYMK-RGLSVWLDPDLALARRIAKVTASRPL 213
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DB    72 ILRKLSNEDK-IATGTGGIVQSARENRRFLKTQFIVLYLEAADCLVDRIQQDETISRPL 129

RESULT 7
US-09-583-110-3547
; Sequence 3547, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583.110

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; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3547
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3547

Query Match 11.7%; Score 179; DB 4; Length 158;
Best Local Similarity 34.8%; Pred. No. 5.5e-11;
Matches 62; Conservative 27; Mismatches 63; Indels 26; Gaps 8

Qy 98 LVYMGSGKSTVGKIMSEVLGYSGFSDSKLVEQAVGHPVAQIFKVHSEAFPRDNESVYL 257
Db 5 LLGFNGAGKSTIAR---GLDTNYLDMDALIERKLG-M-STANPFAEKGEETFRQVESEVL 59
Qy 158 RDLSSMRRLVATGGGAVIRPINRYMKRGL-SVWLDVPLDALARRIAKTAVGTASRRPLDQ 216
Db 60 ALLQTDQ-VVSTGGGVVISQRNDDLKTNDNYLKADFTYIQRIAADKONQRPFLN 118
Qy 217 PSGDPYAFKSLSLAQORQDAYANADRVRSLEEIAKQGHGDDVSKLTPDTIAESL 274
Db 119 NSKE-----ELVAIFERQAWY-----EEVASRV--LDVTKLSPEEI-IEEL 157

RESULT 8
US-09-107-433-3398
; Sequence 3398, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3398:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 159 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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149 FRDNSSVLRDLSSMRRLVWATGGCAVTRPINRWYK-RGLSVWLDVPLDALARRIAKVG 207
167 FSECEARILETLPEDAL-LSLGGTLLMYEASRAIOTRGALVFLSVLPLIYERLEKRG 125
208 TASRPLLDPSGDPYMAFSLKSLMAQOQRGDAYANADVRSLEEIACKQGHDDVSKLTPT 267
226 LPER-LKE-----AMTKPLSEILTERID-----RMKEIA-----DYI----- 157
268 DIAIESLHKIESFVIEHTADSSASDAQAESQ 298
358 -----FPVDHVDHSSKSSLEQASQ 176

RESULT 14
US-09-134-001C-3610
; Sequence 3610, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLAIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPH
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3610
; LENGTH: 172
; TYPE: ERT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3610

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Best Local Similarity 28.9%; Pred. NO. 7.9e-07;
Matches 46; Conservative 31; Mismatches 73; Indels 9; Gaps
Qy 96 IYLVMGMSGKSTGKIMSEVLGYSFPDSDKLVEQAGVMPSSVAQIFKVHSEAFFRDNESS 155
Db 10 IILVGFMTGKTTVGKLSLDYLNLSYVDLDNFIE-VNECKSIPNIFNDIGEGFRSLETR 68
Qy 156 VLRLDSMRRL-VVATGGGAVIRPINWRMYMKRGLS-VWLDVPLDALARRIAKVGTASRPL 213
Db 69 YLK--SCLNTFDIISTGGIIEDTNSLLKLLKQKHVVWLDCCDIEIIFKRVK--NDSHRPN 124
Qy 214 LDQSPGDPYAMAFSKLSMLAQOQGDYANADVRSLEEI 252
Db 125 AKSNLNQLDALYS--SRLSRYNEIAFMKVDSQAQSVSEI 161

RESULT 15
US-09-248-796A-18195
; Sequence 18195, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keitch Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDI
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18195

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; LENGTH: 276
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18195

Query Match      8.2%; Score 125; DB 4; Length 276;
Best Local Similarity 26.4%; Pred. No. 7.2e-05;
Matches 33; Conservative 28; Mismatches 44; Indels 20; Gaps 4;

QY 56 LRLRAKKSSGGHE---NSHNSVDEALLLXKXSEEVLPYLNRCIYLVGNMGSKGSTVGKI 112
Db 72 LHSKFKEIDGYEPPPTDKHVDK-----SDKSIIVIGMRGTGKSTLSEW 117

QY 113 MSEVLGYSFFDSKLVQAVGMPVAQIFKVHSEAFPRDNESSVLRDLSS--MRRLVAVT 170
Db 118 LASFLGFKMLDMDKYLEEKLG-TGIKSLIKAKGWYFROEBAIVAKCEFTKFSKGYVLST 176

QY 171 GGGAV 175
Db 177 GGGIV 181
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Search completed: August 25, 2005, 11:17:53
Job time : 23 secs

QY 61 KKSSGGHSHNSVDDEALLKKRSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 120
Db 61 KKSSGGHSHNSVDDEALLKKRSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 120
QY 121 FFDSDKLVEQAVGMPVAQIFKVHSEAFPRDNESVLRDLSSMRRLVAVATGGGAVIRPIN 180
Db 121 FFDSDKLVEQAVGMPVAQIFKVHSEAFPRDNESVLRDLSSMRRLVAVATGGGAVIRPIN 180
QY 181 WRYMKRGLSVLWLDVPLDALARRIAKVGTASRPDLDPSPGDPYAMAFSKLSMLAQQRGDY 240
Db 181 WRYMKRGLSVLWLDVPLDALARRIAKVGTASRPDLDPSPGDPYAMAFSKLSMLAQQRGDY 240
QY 241 ANADVRSLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 300
Db 241 ANADVRSLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 300
QY 301 RIQTL 305
Db 301 RIQTL 305

RESULT 2
US-10-425-114-69542
; Sequence 69542, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69542
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73062D01_FLI.pap
US-10-425-114-69542

Query Match 100.0%; Score 1526; DB 15; Length 314;
Best Local Similarity 100.0%; Pred. No. 7.1e-141;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEAGGVGLALQARAAGFGSSRRHGGLOAPTGSRLRVADPAGPAVAVRARGSKPVAPLRLRA 60
Db 10 MEAGGVGLALQARAAGFGSSRRHGGLOAPTGSRLRVADPAGPAVAVRARGSKPVAPLRLRA 69
QY 61 KKSSGGHSHNSVDDEALLKKRSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 120
Db 70 KKSSGGHSHNSVDDEALLKKRSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 129
QY 121 FFDSDKLVEQAVGMPVAQIFKVHSEAFPRDNESVLRDLSSMRRLVAVATGGGAVIRPIN 180
Db 130 FFDSDKLVEQAVGMPVAQIFKVHSEAFPRDNESVLRDLSSMRRLVAVATGGGAVIRPIN 189
QY 181 WRYMKRGLSVLWLDVPLDALARRIAKVGTASRPDLDPSPGDPYAMAFSKLSMLAQQRGDY 240
Db 190 WRYMKRGLSVLWLDVPLDALARRIAKVGTASRPDLDPSPGDPYAMAFSKLSMLAQQRGDY 249
QY 241 ANADVRSLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 300
Db 250 ANADVRSLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 309
QY 301 RIQTL 305
Db 310 RIQTL 314

RESULT 3
US-10-425-115-201135
; Sequence 201135, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201135
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115020C.1.pap
US-10-425-115-201135
Query Match 95.5%; Score 1457; DB 16; Length 303;
Best Local Similarity 96.1%; Pred. No. 4e-134;
Matches 293; Conservative 2; Mismatches 8; Indels 2; Gaps 1;
QY 1 MEAGGVGLALQARAAGFGSSRRHGGLOAPTGSRLRVADPAGPAVAVRARGSKPVAPLRLRA 60
Db 1 MEAGGVGLALQARAAGFGSSRRHGGLOAPTGSRLRVADPAGPAVAVRARGSKPVAPLRLRA 58
QY 61 KKSSGGHSHNSVDDEALLKKRSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 120
Db 59 KKSSGGHSHNSVDDEALLKKRSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 118
QY 121 FFDSDKLVEQAVGMPVAQIFKVHSEAFPRDNESVLRDLSSMRRLVAVATGGGAVIRPIN 180
Db 119 FFDSDKLVEQAVGMPVAQIFKVHSEAFPRDNESVLRDLSSMRRLVAVATGGGAVIRPIN 178
QY 181 WRYMKRGLSVLWLDVPLDALARRIAKVGTASRPDLDPSPGDPYAMAFSKLSMLAQQRGDY 240
Db 179 WRYMKRGLSVLWLDVPLDALARRIAKVGTASRPDLDPSPGDPYAMAFSKLSMLAQQRGDY 238
QY 241 ANADVRSLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 300
Db 239 ANADVRSLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 298
QY 301 RIQTL 305
Db 299 RIQTL 303

RESULT 4
US-10-425-115-201137
; Sequence 201137, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201137
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Zea mays
US-10-425-115-201137
Query Match 100.0%; Score 1526; DB 15; Length 314;
Best Local Similarity 100.0%; Pred. No. 7.1e-141;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEAGGVGLALQARAAGFGSSRRHGGLOAPTGSRLRVADPAGPAVAVRARGSKPVAPLRLRA 60
Db 10 MEAGGVGLALQARAAGFGSSRRHGGLOAPTGSRLRVADPAGPAVAVRARGSKPVAPLRLRA 69
QY 61 KKSSGGHSHNSVDDEALLKKRSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 120
Db 70 KKSSGGHSHNSVDDEALLKKRSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 129
QY 121 FFDSDKLVEQAVGMPVAQIFKVHSEAFPRDNESVLRDLSSMRRLVAVATGGGAVIRPIN 180
Db 130 FFDSDKLVEQAVGMPVAQIFKVHSEAFPRDNESVLRDLSSMRRLVAVATGGGAVIRPIN 189
QY 181 WRYMKRGLSVLWLDVPLDALARRIAKVGTASRPDLDPSPGDPYAMAFSKLSMLAQQRGDY 240
Db 190 WRYMKRGLSVLWLDVPLDALARRIAKVGTASRPDLDPSPGDPYAMAFSKLSMLAQQRGDY 249
QY 241 ANADVRSLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 300
Db 250 ANADVRSLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 309
QY 301 RIQTL 305
Db 310 RIQTL 314

; FEATURE:
; OTHER INFORMATION: Clone ID: MR74577_115022C.1.pcp
US-10-425-115-201137

Query Match 90.9%; Score 1387; DB 16; Length 303;
Best Local Similarity 91.1%; Pred. No. 3e-127; Mismatches 16; Indels 2; Gaps 1;
Matches 278; Conservative 9;
QY 1 MEAGGVGLALQARAAGFSSRRHGGIQAPTGSLRVADPAGPAAVAVRARGSKPVAPLRLRA 60
DB 1 MEAGGVGLALQTRAAGFSGQRGGIQAPTGSLRVADPAGPAAVAVRARGSKPVAPLRLRA 58
QY 61 KKSOGGSHNSVDEALLKRSSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 120
DB 59 KKSOGGSHNSVDEALLKRSSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 118
QY 121 FFDSDKLVEQAVGMPVAQIFKVHSEAFRDNESSVLRDLSSMRRLVAVATGGAVIRPIN 180
DB 119 FFDSDKLVEQAVGMPVAQIFKVHSEAFRDNESSVLRDLSSMRRLVAVATGGAVIRPIN 178
QY 181 WRYMKRGLSVMLDVPDLALARRIAKVGTAASRPLLDQPSGDPYMAFASKLSMLAQORGDAY 240
DB 179 WKYMKKGLSVMLDVPDLALARRIAKVGTAASRPLLDQPSGDPYMAFASKLSMLAQORGDAY 238
QY 241 ANADVRVSLLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 300
DB 239 ANADVRVSLLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 298
QY 301 RIQTL 305
DB 299 RIQTL 303

RESULT 5

US-10-425-114-62604
; Sequence 62604, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62604
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:

; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE77E09_FLI.pcp
US-10-425-114-62604

Query Match 90.9%; Score 1387; DB 15; Length 324;
Best Local Similarity 91.1%; Pred. No. 3.3e-127;
Matches 278; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

QY 1 MEAGGVGLALQARAAGFSSRRHGGIQAPTGSLRVADPAGPAAVAVRARGSKPVAPLRLRA 60
DB 22 MEAGGVGLALQTRAAGFSGQRGGIQAPTGSLRVADPAGPAAVAVRARGSKPVAPLRLRA 79
QY 61 KKSOGGSHNSVDEALLKRSSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 120
DB 80 KKSOGGSHNSVDEALLKRSSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 139
QY 121 FFDSDKLVEQAVGMPVAQIFKVHSEAFRDNESSVLRDLSSMRRLVAVATGGAVIRPIN 180
DB 140 FFDSDKLVEQAVGMPVAQIFKVHSEAFRDNESSVLRDLSSMRRLVAVATGGAVIRPIN 199

QY 181 WRYMKRGLSVMLDVPDLALARRIAKVGTAASRPLLDQPSGDPYMAFASKLSMLAQORGDAY 240
DB 200 WKYMKKGLSVMLDVPDLALARRIAKVGTAASRPLLDQPSGDPYMAFASKLSMLAQORGDAY 259
QY 241 ANADVRVSLLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 300
DB 260 ANADVRVSLLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 319
QY 301 RIQTL 305
DB 320 RIQTL 324

RESULT 6

US-10-425-114-57834
; Sequence 57834, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57834
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:

; OTHER INFORMATION: Clone ID: UC-ZMFLB73191D05_FLI.pcp
US-10-425-114-57834

Query Match 90.9%; Score 1387; DB 15; Length 326;
Best Local Similarity 91.1%; Pred. No. 3.3e-127;
Matches 278; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

QY 1 MEAGGVGLALQARAAGFSSRRHGGIQAPTGSLRVADPAGPAAVAVRARGSKPVAPLRLRA 60
DB 24 MEAGGVGLALQTRAAGFSGQRGGIQAPTGSLRVADPAGPAAVAVRARGSKPVAPLRLRA 81
QY 61 KKSOGGSHNSVDEALLKRSSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 120
DB 82 KKSOGGSHNSVDEALLKRSSEVLFYLNRCIYLVGMGSGKSTVGKIMSEVLGYS 141
QY 121 FFDSDKLVEQAVGMPVAQIFKVHSEAFRDNESSVLRDLSSMRRLVAVATGGAVIRPIN 180
DB 142 FFDSDKLVEQAVGMPVAQIFKVHSEAFRDNESSVLRDLSSMRRLVAVATGGAVIRPIN 201
QY 181 WRYMKRGLSVMLDVPDLALARRIAKVGTAASRPLLDQPSGDPYMAFASKLSMLAQORGDAY 240
DB 202 WKYMKKGLSVMLDVPDLALARRIAKVGTAASRPLLDQPSGDPYMAFASKLSMLAQORGDAY 261
QY 241 ANADVRVSLLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 300
DB 262 ANADVRVSLLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ 321
QY 301 RIQTL 305
DB 322 RIQTL 326

RESULT 7

US-10-767-701-44984
; Sequence 44984, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:

```
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 44984
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C10471_1.pep
US-10-767-701-44984

Query Match      88.6%; Score 1351.5; DB 16; Length 330;
Best Local Similarity 83.3%; Pred. No. 1e-123;
Matches 279; Conservative 8; Mismatches 13; Indels 35; Gaps 3;

QY 1 MEAGGVGLALQAR-----AAGFGSSRRHGGLOAPT 30
   |||||
Db 1 MEA---GLAQTRAAGFGSGRRRGGQLSPIGSLRVADPAGAAVAAGFGSGRRRGGQLSP 57
   |||||

QY 31 GSLRVADPAGPAAVARGSKPVAPLRLRAKSSGGHSHNSVDEALLLKRKSEVLFPY 90
   |||||
Db 58 GSLRVADPAGAAVAVARGSKPVAP--LRKKSFGGHENLHNSVDEALLLKRKSEVLFPY 115
   |||||

QY 91 LNGRCIYLVGMGSGKSTVGKIMSEVLGYSPFSDSKLVEQAVGMPMSVAQIFKVHSEAPPR 150
   |||||
Db 116 LNGRCIYLVGMGSGKSTVGKIMSEVLGYSPFSDSKLVEQAVGMPMSVAQIFKVHSEAPPR 175
   |||||

QY 151 DNESSVLRDLSSMRRLVATGGGAVIRPINWRYMKRGLSVLDVPLDALARRIAKVGTAS 210
   |||||
Db 176 DNESSVLRDLSSMRRLVATGGGAVIRPINWRYMKRGLSVLDVPLDALARRIAKVGTAS 235
   |||||

QY 211 RPLDQPSGDPYAMAFSKLSMLAQORGDAYANADVRSLEETACKQGHDDVSKLTPTDIA 270
   |||||
Db 236 RPLDQPSGDPYTMAFSKLSMLAEQORGDAYANADVRSLEETACKQGHDDVSKLTPTDIA 295
   |||||

QY 271 IESLHKIESFVIEHTADSSASDAQESQIQRIQTL 305
   |||||
Db 296 IESLHKIESFVSEHTPDNPASDSQAESQIQRIQTL 330
   |||||

RESULT 8
US-10-437-963-147803
; Sequence 147803, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147803
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48297C.1.pap
US-10-437-963-147803
```

```
Query Match      85.3%; Score 1301.5; DB 16; Length 308;
Best Local Similarity 86.2%; Pred. No. 7.4e-119;
Matches 268; Conservative 13; Mismatches 21; Indels 9; Gaps 4;

QY 1 MEAGGVGLALQARAGF--GSSRRHGGGL-----QAPTGSLRVADPAGPAAVAVARGSKPVA 54
   |||||
Db 1 MEA-CVGLALQSLRAAGFGSDRRRSALYGGEGRAGRIGSLRVAEPAAKAAVAVARGSKPVA 59
   |||||

QY 55 PLRLRAKSSGGHSHNSVDEALLLKRKSEVLFPYLNRCIYLVGMGSGKSTVGKIMS 114
   |||||
Db 60 P--LRKKSFGGHETLHNSVDEALLLKRKSEVLFPYLNRCIYLVGMGSGKSTVGKIMS 117
   |||||

QY 115 EVLGYSPFSDSKLVEQAVGMPMSVAQIFKVHSEAPPRDNESSVLRDLSSMRRLVATGGGA 174
   |||||
Db 118 EVLGYSPFSDSKLVEQAVGMPMSVAQIFKVHSEAPPRDNESSVLRDLSSMRRLVATGGGA 177
   |||||

QY 175 VIRPINWRYMKRGLSVLDVPLDALARRIAKVGTASRPLDQPSGDPYAMAFSKLSMLAQ 234
   |||||
Db 178 VIRPINWRYMKRGLSVLDVPLDALARRIAKVGTASRPLDQPSGDPYTMAFSKLSMLAE 237
   |||||

QY 235 ORGDAYANADVRSLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQ 294
   |||||
Db 238 ORGDAYANADVRSLEETACKQGHDDVSKLTPTDIAIESFHKIENFVIEHTVDNPVGSQ 297
   |||||

QY 295 AESQIQRIQTL 305
   ||:|
Db 298 ADSRAQRIQTL 308
   ||:|

RESULT 9
US-10-660-226-28
; Sequence 28, Application US/10660226
; Publication No. US20040064848A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, S. Carl
; APPLICANT: Pamodu, Lavo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Rendina, Alan
; TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
; FILE REFERENCE: BB-1159-C
; CURRENT APPLICATION NUMBER: US/10/660,226
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/09/354,501
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 28
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-660-226-28

Query Match      76.0%; Score 1159; DB 15; Length 273;
Best Local Similarity 85.5%; Pred. No. 6e-105;
Matches 235; Conservative 17; Mismatches 17; Indels 6; Gaps 3;

QY 32 SLRVADPAGPAAVAVARGSKPVAPLRLRAKKS--GGHSHNSVDEALLLKRKSEVLFPY 90
   |||||
Db 4 SLRVSDLVGSPAAVARGAKPVP--LRKKSFGGHENLHNSVDDALLLKRKSEVLFPQ 61
   |||||

QY 91 LNGRCIYLVGMGSGKSTVGKIMSEVLGYSPFSDSKLVEQAVGMPMSVAQIFKVHSEAPPR 150
   |||||
Db 62 LNGRCIYLVGMGSGKSTVGKILAEVLGYSPFSDSKLVEQAVGMPMSVAQIFKVHSEAPPR 121
   |||||

QY 151 DNESSVLRDLSSMRRLVATGGGAVIRPINWRYMKRGLSVLDVPLDALARRIAKVGTAS 210
   |||||
Db 122 DNESSVLRDLSSMRRLVATGGGAVIRPINWRYMKRGLSVLDVPLEALARRIAKVGTAS 181
   |||||

QY 211 RPLDQPSGDPYAMAFSKLSMLAQORGDAYANADVRSLEETACKQGHDDVSKLTPTDIA 270
   |||||
```

Db 182 RPLDQPSGDPYTMAPSKLSMLAEQRGDAYANADVRSLEETASKLGHDDVSKLTPIDIA 241

Qy 271 IESLHKIESFVIEHTWADSSADAQAEQIQTQL 305

Db 242 LESLHKIESFVVE---DTAVADSQIESQSRMHTL 273

RESULT 10

US-10-425-115-201136

Sequence 201136, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 201136

LENGTH: 217

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(217)

OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_115021C.1.pap

US-10-425-115-201136

Query Match 69.5%; Score 1061; DB 16; Length 217;

Best Local Similarity 98.6%; Pred. No. 1.8e-95;

Matches 212; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEAGGVGLALQARAGFGSSRRHGGIQAPTGSLRVADPAGPAVAVRARGSKPVALRLRA 60

Db 1 MEAGGVGLALQARAGFGSSRRHGGIQAPTGSLRVADPAGPAVAVRARGSKPVALRLRA 60

Qy 61 KXSSGSHNSHNSVDEALLKKRSEVLYFLNGRCIYLVGMGSGKSTVGKIMSEVLGYS 120

Db 61 KXSSGSHNSHNSVDEALLKKRSEVLYFLNGRCIYLVGMGSGKSTVGKIMSEVLGYS 120

Qy 121 PFDSKLVQAVGMPMSVAQIFKVHSEAFPRDNESVRLDSSMRRLVWATGGAVIRPIN 180

Db 121 PFDSKLVQAVGMPMSVAQIFKVHSEAFPRDNESVRLDSSMRRLVWATGGAVIRPIN 180

Qy 181 WRYMKRGLSVWLDVPLDALARRIAKVGTASRPLLD 215

Db 181 WRYMKRGLSVWLDVPLDALARRIAKVGTASRPLLD 215

RESULT 11

US-10-437-963-187425

Sequence 187425, Application US/10437963

Publication No. US2004023343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 187425

LENGTH: 311

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_84129C.1.pap

US-10-437-963-187425

Query Match 58.1%; Score 886; DB 16; Length 311;

Best Local Similarity 59.8%; Pred. No. 4.5e-78;

Matches 202; Conservative 27; Mismatches 49; Indels 60; Gaps 9;

Qy 1 MEAGGVGLALQARAA-GFGSS---RHRGGLQAPTG-SLRVADPAG-----PAVA 44

Db 1 MEA-RAGLAMQRAAAGVGAGPGVGRGRARDPRGEAANRGPAGRRPRRTGGGQAPRA 59

Qy 45 VRARG-----SKPVAPLRLRAKSS-----GGHSHNSVDEALLKKRSEVLY 88

Db 60 VLPQGVQSFLIGLGEVVTFFVWISKDNLCNVGVNGVVGQHDLSHNSVDEALLKKRSEVLY 119

Qy 89 FYLNGRCIYLVGMGSGKSTVGKIMSEVLGYSFFDSKLVQAVGMPMSVAQIFKVHSEAF 148

Db 120 FYLNGRCIYLVGMGSGKSTVAKILAEVLGYSFFDSKLVQAVGMPMSVAQIFKVHSEAF 179

Qy 149 FRDNESVRLDSSMRRLVWATGGAVIRPINWRYMKRGLSVWLDVPLDALARRIAKVGT 208

Db 180 FRDNEA-----MKYMKRGLSVWLDVPLDALARRIAKVGT 213

Qy 209 ASRPLDQPSGDPYAMAFSKLSMLAQQRDAYANADVRSLEETACKQGHDDVSKLTPTD 268

Db 214 ASRPLDQPSGDPYTAAFSKLSMLAEQQRDAYANADVRSLEETAAKQGHDDVSKLTPTD 273

Qy 269 IAISLHKIESFVIEH-TADSSASDAQAESQIQIOTL 305

Db 274 IAIEALLKIENFVTEHSTSSGPGVDLIVDSQVRRTKAL 311

RESULT 12

US-10-660-226-26

Sequence 26, Application US/10660226

Publication No. US20040064848A1

GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Falco, S. Carl

APPLICANT: Famodu, Layo O.

APPLICANT: Hitz, William D.

APPLICANT: Rendina, Alan

TITLE OF INVENTION: Chorismate Biosynthesis Enzymes

FILE REFERENCE: BB-1159-C

CURRENT APPLICATION NUMBER: US/10/660,226

CURRENT FILING DATE: 2003-09-11

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US/09/354,501

PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Microsoft Office 97

SEQ ID NO 26

LENGTH: 282

TYPE: PRT

ORGANISM: Triticum aestivum

US-10-660-226-26

Query Match 57.3%; Score 874; DB 15; Length 282;

Best Local Similarity 65.2%; Pred. No. 5.9e-77;

Matches 180; Conservative 33; Mismatches 49; Indels 14; Gaps 2;

Qy 22 HRGGLQAPTGSLRVADPAG-----GPVAVRARGSKPVALRLRAKSS-----SGGH 67

Db 1 HEAKRKQGGFPFATVPVAVRLDQNPARRPLVRLTDAGSRSTDPIGASIKALCCHKSAGT 60

Qy 68 ENSHNSVDEALLKKRSEVLYFLNGRCIYLVGMGSGKSTVGKIMSEVLGYSFFDSOKL 127

Db 61 EKAHYSADAEALVLKQAEVDLPYLNDRCVYLVGMGSGKTTVGKIIAEVLGYSFDFSDKL 120
QY 128 VEQAVGMPVAQIFKVHSEAFPRDNESVLRDLSSMRRLVATGGGAVIRPINWRYMKRG 187
Db 121 VEQSGVIPSVAEIFQVHSEAFPRDNESVLRDLSSMRRLVATGGGAVIRPINWRYMKRG 180
QY 188 LSVLWLDVPLDALARRIAVGTASRPLDHQESGDPYAKAYAKLTAUFQRMDSYANADARV 247
Db 181 LTIWLDVPLDALARRIAVGTASRPLDHQESGDPYAKAYAKLTAUFQRMDSYANADARV 240
QY 248 SLEETACKQGHDDVSKLTPTDIAIESLHKIESFVIE 283
Db 241 SLENTAFKQGHDDVNVLTSAIAIEALLKQESFLTE 276

RESULT 13
US-10-660-226-20
; Sequence 20, Application US/10660226
; Publication No. US20040064848A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Lavo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Rendina, Alan
; TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
; FILE REFERENCE: BB-1159-C
; CURRENT APPLICATION NUMBER: US/10/660,226
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/09/354,501
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Sorghum
US-10-660-226-20

Query Match 56.4%; Score 860; DB 15; Length 245;
Best Local Similarity 70.4%; Pred. No. 1.1e-75;
Matches 174; Conservative 32; Mismatches 33; Indels 8; Gaps 2;
QY 39 AGPAVAVRARGSKPVAPLRRAKSSGGHSHNSVDEALLKRSSEVLPYLNDRCVYL 98
Db 3 AGPAL-----RP-AKLAVSCSAKSAGTGKHYSTDEALILQKQAQDVLPLDGRVCYL 54
QY 99 VGMGSGKSTVGKIMSEVLGYSEFFSDKLVEQAVGMPVAQIFKVHSEAFPRDNESVLR 158
Db 55 VGMGSGKSTVGKILAEVLGYSEFFSDKLVEQAVGMPVAQIFKVHSEAFPRDNESVLR 114
QY 159 DLSSMRRLVATGGGAVIRPINWRYMKRLSVLWLDVPLDALARRIAVGTASRPLDHQES 218
Db 115 DLSSMRRLVATGGGAVIRPINWRYMKRLSVLWLDVPLDALARRIAVGTASRPLDHQES 174
QY 219 GOPYAMAFSKLSMLAQORGDYANADRVSLBEIAKQGHDDVSKLTPTDIAIESLHKIE 278
Db 175 GOPYAMAFSKLSLQORGDYANADRVSLBEIAKQGHDDVSKLTPTDIAIESLHKIE 234
QY 279 SFVIEHT 285
Db 235 SFLTEXT 241

RESULT 14
US-10-425-115-253534
; Sequence 253534, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 253534
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_162804C.1.pep
US-10-425-115-253534

Query Match 56.2%; Score 858; DB 16; Length 292;
Best Local Similarity 66.8%; Pred. No. 2.3e-75;
Matches 173; Conservative 34; Mismatches 52; Indels 0; Gaps 0;
QY 27 QAPTGSRLVADPAGPAVAVRARGSKPVAPLRRAKSSGGHSHNSVDEALLKRSSE 86
Db 30 RVPTARLAVAADRPRLVLLGADTERRAADPALRCAAQASAGTGKHYSDADALILQKQAQD 89
QY 87 VLPYLNDRCVYLVGMGSGKSTVGKIMSEVLGYSEFFSDKLVEQAVGMPVAQIFKVHSE 146
Db 90 VLPYLDGRVCYLWGMGSGKTTVGKILSEVLGYSEFFSDKLVEQAVGMPVAQIFKVHSE 149
QY 147 AFFRDNESVLRDLSSMRRLVATGGGAVIRPINWRYMKRLSVLWLDVPLDALARRIAK 206
Db 150 TFFRDNESVLRDLSSMRRLVATGGGAVIRPINWRYMKRLSVLWLDVPLDALARRIAK 209
QY 207 GTASRPLDHQESGDPYAMAFSKLSMLAQORGDYANADRVSLBEIAKQGHDDVSKLTPT 266
Db 210 GTASRPLDHQESGDPYAMAFSKLSMLAQORGDYANADRVSLBEIAKQGHDDVSKLTPT 269
QY 267 TDIAIESLHKIESFVIEHT 285
Db 270 STIAIEALLKQESFLTEXT 288

RESULT 15
US-10-660-226-12
; Sequence 12, Application US/10660226
; Publication No. US20040064848A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Lavo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Rendina, Alan
; TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
; FILE REFERENCE: BB-1159-C
; CURRENT APPLICATION NUMBER: US/10/660,226
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/09/354,501
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Zea mays
US-10-660-226-12

Query Match 55.1%; Score 841; DB 15; Length 231;
Best Local Similarity 73.7%; Pred. No. 7.6e-74;
Matches 165; Conservative 31; Mismatches 28; Indels 0; Gaps 0;
QY 62 KSSGGHSHNSVDEALLKRSSEVLPYLNDRCVYLVGMGSGKSTVGKIMSEVLGYSF 121

Db 4 Q SAGGTGKVHYSADDA L I I Q Q K A Q D V L P Y L D G R C V Y L V G M M G S G K T T V G K I L S E V L G Y S F 63
Qy 122 F D S D K L V E Q A V G M P S V A Q I F K V H S E A F F R D N E S S V L R D L S S M R R L V V A T G G G A V I R P I N W 181
Db 64 F D S D K L V E K A V G I S S V A E I F Q L H S E T F F R D N E S E V L T D L S S M H R L V V A T G G G A V I R P I N W 123
Qy 182 R Y M K R G L S V W L D V P L D A L A R R I A K V G T A S R P L L D Q P S G D P Y A M A F S K L S M L A Q Q R G D A Y A 241
Db 124 S Y M K G L T V W L D V P L D A L A R R I A A V G T A S R P L L H Q E S G D P Y A K A Y A K L T S L F E Q R M D S Y A 183
Qy 242 N A D V R V S L E E I A C K Q G H D D V S K L T P T D I A E S L H K I E S F V I E H T 285
Db 184 N A D A R V S L E H I A L K Q G H N D V T I L T P S T I A I E A L L K M E S F L T E K T 227

Search completed: August 25, 2005, 11:19:05
Job time : 67 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 25, 2005, 19:08:37 ; Search time 4914 Seconds
(without alignments)

3007.497 Million cell updates/sec

Title: US-10-660-226-10

Perfect score: 1526

Sequence: 1 MEAGVGGLQARAAAGFGSS.....ADSSASDAQESQIQRIQTL 305

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=xlh

-Q=/cgn2_1/USFTO_spool/US10660226/runat_25082005_110427_28529/app_query.fasta_1.455

-DB=GenEmbl -QFMT=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US10660226 @CNC 1.1 3731 @runat_25082005_110427_28529 -NCFU=6 -ICPU=3

-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.ste.*

12: gb.sv.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1162.5	76.2	1356	8 AK066687	Oryza sat
2	1159	76.0	1061	8 BT009529	Triticum
3	1025.5	67.2	1918	8 AK109730	Oryza sat
4	881.5	57.8	1323	8 BT009514	Triticum

C	5	836.5	54.8	111777	2	AP004089	Oryza sat
	6	836.5	54.8	154796	8	AP004774	Oryza sat
	7	836.5	54.8	155168	8	AP005848	Oryza sat
C	8	733	48.0	137319	8	AP003513	Oryza sat
	9	697.5	45.7	2127	8	AK067948	Oryza sat
	10	691	45.3	1167	8	AK070318	Oryza sat
	11	655	42.9	1300	8	AK118899	Arabidops
	12	642.5	42.1	1293	8	LESHKINP	X63560 L.esculentu
	13	642.5	42.1	1303	8	BT012939	Lycopersi
	14	606.5	39.7	903	8	BT005291	Arabidops
	15	606.5	39.7	1294	8	AK117791	Arabidops
C	16	516.5	33.8	126659	8	OSUN00015	Arabidops
C	17	516.5	33.8	155576	2	OSUN00094	Oryza sat
	18	459.5	30.1	107848	8	AC007019	Arabidops
	19	440	28.8	1016	8	AY596190	Cucumis s
	20	390	25.6	129047	8	ATF23K16	Arabidops
	21	390	25.6	198151	8	ATCHRIV91	Arabidops
	22	374	24.5	309	6	AX315616	Sequence
	23	357	23.4	297850	1	AP006577	Gloebact
	24	340.5	22.3	306803	1	AE017161	Prochloro
	25	340.5	22.3	342050	1	AP003585	Nostoc sp
	26	331.5	21.7	843	8	BT012407	Arabidops
	27	331.5	21.7	898	8	BT012132	Arabidops
C	28	321.5	21.1	344615	1	BX569695	Synechoco
	29	321	21.0	137740	1	D90900	Synechocyst
	30	311.5	20.4	300450	1	AP005371	Thermosyn
	31	301	19.7	110000	2	AP006502_02	Continuation (3 of
C	32	285	18.7	349391	1	BX572095	Prochloro
	33	272.5	17.9	349742	1	BX572090	Prochloro
C	34	268.5	17.6	300600	1	AP005935	Bradyrhiz
C	35	262	17.2	110000	1	AE017180_22	Continuation (23 o
	36	256.5	16.8	348971	1	BX572594	Rhodospseu
C	37	254.5	16.7	110000	1	BX897699_18	Continuation (19 o
	38	254	16.6	5062	14	SVU27645	Sealth vir
C	39	252.5	16.5	110000	1	AP006840_20	Continuation (21 o
	40	250	16.4	81384	1	AB897700_15	Continuation (16 o
	41	249.5	16.3	15580	1	AE000776	Aquifex a
	42	246	16.1	1125	8	AK064812	Oryza sat
	43	245	16.1	696	6	AR449503	Sequence
	44	245	16.1	14335	6	AR408732	Sequence
	45	245	16.1	14335	6	AX067436	Sequence

ALIGNMENTS

RESULT 1	AK066687	Oryza sativa (japonica cultivar-group)	1356 bp	mRNA	linear	PLN 24-JUL-2003
LOCUS	AK066687	Oryza sativa (japonica cultivar-group)	1356 bp	mRNA	linear	PLN 24-JUL-2003
DEFINITION	AK066687	Oryza sativa (japonica cultivar-group)	1356 bp	mRNA	linear	PLN 24-JUL-2003
ACCESSION	AK066687.1	GI:32976705				
VERSION	AK066687					
KEYWORDS	FLI_CDNA; CAP trapper.					
SOURCE	Oryza sativa (japonica cultivar-group)					
ORGANISM	Oryza sativa (japonica cultivar-group)					
REFERENCE	1	Oryza sativa (japonica cultivar-group)				
AUTHORS	1	Oryza sativa (japonica cultivar-group)				
	1	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.				

The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team:
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Hotta,I., Kodama,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuka,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ohtsuka,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niihara,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Mura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN, Kawai,J., Carninci,P., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,

Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

Science 301 (5631), 376-379 (2003)

22752273

12869764

2 (bases 1 to 1356)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Iehikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kuroaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yanagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,

Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,

Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,

Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,

Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center

and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,

Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,

Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,

Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,

Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oota, N.,

Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,

Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,

Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,

Yasunishi, A. and Hayashizaki, Y.

Location/Qualifiers

1. .1356

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="J013074E04"

FEATURES
source

ORIGIN

Alignment Scores:

Pred. No.: 1356
Score: 1162.50
Length: 1356
Matches: 259
Percent Similarity: 71.02%
Conservative: 13
Best Local Similarity: 67.62%
Mismatch: 22
Query Match: 76.18%
Indels: 90
DB: 6
Gaps: 6

US-10-660-226-10 (1-305) x AK066687 (1-1356)

QY 1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAlaAlaGlyPhe---GlySer 19
Db 81 ATGAGGGG---GGCGTGGGGTGGCGTGGCGGGGGGGGGTTCGGCGGCTCC 137
QY 20 SerArgHisArgGlyGlyLeu-----GlnAlaProThrGlySerLeuArg 34
Db 138 GACCCGCCCGGAGGCGCTCTACGGCGCGGCGGCGCGGATCGGAGGCTTGAGG 197
QY 35 ValAlaAspProAlaGlyProAlaValAlaValArgAlaArgGlySerLysProValAla 54
Db 198 GTGCGTGGAGCGCGGTGGCGAGAGCGCGTGTGTGGGCTCGCGGTCGAAGCGGTCGCC 257
QY 55 ProLeuArgLeuArgAlaLysLysSerSerGlyGlyHisGluAsnSerHisAsnSerVal 74
Db 258 CCG-----CTCCGTGCCAAGAAATCGTCCGAGGTCATGAACATTCGCAATCGGTT 311
QY 75 AspGluAlaLeuLeuLysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArg 94
Db 312 GATGAAGGCCCTTCTCTAAGAGAGAAATCAGAAGAAGTCTCTTCTATTGAATGGAGCG 371
QY 95 CysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSer 114
Db 372 TGTATTACCTAGTTGGATGATGGTCTCGAAAAAGTACTGTGGAAAGATCATGTCT 431
QY 115 GluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMet 134
Db 432 GAAGTTTTCGGGTATTTCGTTCTTGATAGTATATAATTTGGTGAACAAGCTGTGGGCGATG 491
QY 135 ProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSer 154
Db 492 CTTTCAGTCGCTCAAAATTTCAAGGTTTCATAGTGAAGCTCTTTTAGGATTAATGAGAGT 551
QY 155 SerValLeuArgAspLeuSerSerMetArgArgLeuValAlaAlaThrGlyGlyGlyAla 174
Db 552 AGTGTCTTGAGGATTTGTCCTCAATGAAGCGATTAGTTGTTGTCTACTGGAGTGGTGTCT 611
QY 175 VallIleArgProIleAsnTrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspVal 194
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QY 214 uAspGlnProSerGlyAspProTyrAlaMetAla----- 225
Db 708 AGATCAACCACTCGTGTATCCATACACATGGT-GACTACTTGGCCCATGAATTTATGCC 766
QY 225 ----- 225
Db 767 ATGCATGAATATGATATTATTATTTCAGATGTAATTTTTTAAATTTTAAATCAGTCAATATAG 826
QY 225 ----- 225
Db 827 GCTCATTCATTCATGTAGAAATGAAACCTGCAAGTATGATCTCGACATCTGCACAC 886
QY 225 ----- 225
Db 887 TGGTAGTGAATTCCTTCATTTTCAGTGTAGTATGAGTTGCTCACTGGATTCTTCTATC 946
QY 226 -----PheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAl 243
Db 947 TTAGGCTTTTCTAAACTCAGCATCTCGCGAGCAAAAGGGGCGATGCTTATGCAANTGC 1006

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QY 243 aAspValArgValSerLeuGluIleAlaCysLysGlnGlyHisAspValSerly 263
DB 1007 TGAATGAGGGTTCTCTTGAAGAGATTGTCATCTAAACAGGGTCATGATGATCGAA 1066
QY 263 sLeuThrProThrAspIleAlaIleGluSerLeuHisLysLysPheValIleG 283
DB 1067 GCTAACACCACTGACATTCGTTAGTCGTTTCATAGATCAGAGATTTGTCAATGA 1126
QY 283 uHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSerGlnIleGlnArgIleG 303
DB 1127 ACATACCGTTGACAACTCCGGTGGTGGTCTCCAGGCTGACTCAGTGTCTCAGAGGATACA 1186
QY 303 nThrLeu 305
DB 1187 GACCTTG 1193

RESULT 2
LOCUS BT009529 1061 bp mRNA linear PLN 20-JUN-2003
DEFINITION Triticum aestivum clone wr1.pk0122.a3:figs, full insert mRNA
sequence.
ACCESSION BT009529
VERSION BT009529.1 GI:32129080
KEYWORDS FLI_CDNA.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 1061)
Tingey,S.V., Walters,P., Powell,W., Dolan,M., Miao,G.-H.,
Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
Direct Submission
Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA

FEATURES
Location/Qualifiers
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/db_xref="taxon:4565"
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ORIGIN
Alignment Scores:
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Score: 1159.00 Matches: 235
Percent Similarity: 91.64% Conservative: 17
Best Local Similarity: 85.45% Mismatches: 17
Query Match: 75.95% Indels: 6
DB: Gaps: 3

US-10-660-226-10 (1-305) x BT009529 (1-1061)
QY 32 SerLeuArgValAlaAspProAlaGlyProAlaValAlaValArgAlaArgGlySerLys 51
DB 11 AGCTTCGGTCACTGATCTGGTGGGTCGCCGGCGCGTGGCGCGCGCGCGCGCGAG 70
QY 52 ProValAlaProLeuArgLeuArgAlaLysLysSerSer---GlyGlyHisGluAsnSer 70
DB 71 CCGGTGCTCCG-----CTCCGCGCACAAGAAATCGTCTGGAGGAGTCTATGAGAATTG 124
QY 71 HisAsnSerValAspGluAlaLeuLeuLysArgLysSerGluLysValLeuPheTyr 90
DB 125 CATAACTCCGTTGACATGCCCTCTGTTGGTGAAGAGAAATCAGAAGAGTCTCTTTCCAG 184
QY 91 LeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGly 110
DB 185 TTGAACGGTGGTGGTCTACCTAGTTGGATGATGGTTCGGGGAAAGTACGTTGGGG 244
QY 111 LysIleMetSerGluValLeuGlyTyrSerPheAspSerAspLysLeuValGluGln 130

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DB 245 AAGATCTTGGCTGAAGATTTTGGTTATTTCATCTTCGACAGTGATAAATTTGGTCGAACA 304
QY 131 AlaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArg 150
DB 305 GCTGTTGGCATGCTTCAGTTGCTCAAAATTTCAAGTTTCATAGTGAAGCCTTCTTCAGA 364
QY 151 AspAsnGluSerSerValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThr 170
DB 365 GATAATGAGAGTAGTGTCTTGAGGAGATTGTCTCAATCGCGGATAGTTGTTGCTACT 424
QY 171 GlyGlyGlyAlaValIleArgProIleAsnTyrArgTyrMetLysArgGlyLeuSerVal 190
DB 425 GGAGTGGTGGTCTGTTATCCGACCGTTAACTGAAAAAATATGAAGAGGGCCTATCTGT 484
QY 191 TrpLeuAspValProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSer 210
DB 485 TGGTTGGATGTCCTTGGAGCTCTTCNAGGCGTATTGCTAAAGTGGGACTGCCTCG 544
QY 211 ArgProLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSer 230
DB 545 CGTCTCTTCTAGATCAACCATCCGGTGATCCATACACAATGGCCTTTTCGAAACTCAGC 604
QY 231 MetLeuAlaGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGlu 250
DB 605 ATGCTCGCGGAGCAAAAGGGCGGATGCTTATGCAAAATGCTGATGTGAGAGTTTCTTCGAA 664
QY 251 GluIleAlaCysLysGlnGlyHisAspValSerLysLeuThrProThrAspIleAla 270
DB 665 GNGATCGCATCTTAAGCTGGTTCATGACCGCTCTTAAGCTGACACCGATTGNTATGCT 724
QY 271 IleGluSerLeuHisLysIleGluSerPheValIleGluHisThrAlaAspSerSerAla 290
DB 725 CTCGAGTGGCTCCACAAGATCGAGAGCTTTGTGCTCGAA-----GACACCGGTGTC 775
QY 291 SerAspAlaGlnAlaGluSerGlnIleGlnArgIleGlnThrLeu 305
DB 776 GCCGAGTCAACAACGGAATCGCAATCTCAAAGGATGCATACCTTG 820

RESULT 3
LOCUS AK109730
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:002-146-B12, full
insert sequence.
ACCESSION AK109730
VERSION AK109730.1 GI:32994939
KEYWORDS FLI_CDNA: oligo capping.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzeae; Oryza.
REFERENCE
1 The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team:,
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group:, Ootomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niihara,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,K., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
JOURNAL Science 301 (5631), 376-379 (2003)
MEDLINE 22752273

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12869764	US-10-660-226-10 (1-305) x AK109730 (1-1918)	
2 (bases 1 to 1918)		
PUBMED		
REFERENCE		
AUTHORS		
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Ikeda, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kusumegi, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsuura, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nishikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Otsu, N., Ota, Y., Otomo, Y., Ryudo, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.		
DIRECT SUBMISSION		
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)		
COMMENT		
This clone is one of the 28K full-length cDNA clones from japonica rice.		
URL : http://cdna01.dna.affrc.go.jp/cDNA/NTAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.		
FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nishikura, J., Oka, M., Ryudo, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsuura, K. and Murakami, K.		
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oota, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.		
LOCATION/QUALIFIERS		
1. .1918		
source		
FEATURES		
BT009514	1323 bp	mRNA linear
LOCUS	BT009514	1323 bp mRNA linear
DEFINITION	Triticum aestivum clone wri.pk0099.b12: fis, full insert mRNA sequence.	PLN 20-JUN-2003
ACCESSION	BT009514	
VERSION	BT009514.1	GI:32129065
KEYWORDS	FLI CDNA.	
SOURCE	Triticum aestivum (bread wheat)	
ORGANISM	Triticum aestivum	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.	
AUTHORS	1 (bases 1 to 1323)	
TITLE	Tingley, S.V., Wolters, P., Powell, W., Dolan, M., Miao, G.-H., Caraher, N.R., Hanafey, M.K. and Hainey, C.F.	
JOURNAL	Direct Submission	
	Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and	

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Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA
FEATURES
  source      Location/Qualifiers
1. .1323      /organism="Triticum aestivum"
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Alignment Scores:
Pred. No.:    2,34e-57      Length:    1323
Score:        881.50       Matches:  183
Percent Similarity: 78.75%   Conservative: 52
Best Local Similarity: 67.03% Mismatches:  32
Query Match:  57.77%      Indels:    6
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Db 22 GCCGCGAGGATCCCCCGCGGACAGTCGCCGGGTGAGCTCGACGAGATCCGGC--- 78
QY 34 ArgValAlaAspProAlaGlyProAla-ValAlaValArgAlaArgGlySerLysProVa 53
    |||||
Db 79 -----CGCGCGCGCGTGTCTCTGCGCACCGGAGCGGGAGCGGACCGATCCCAT 132
QY 53 1-----AlaProLeuArgLeuArgAlaLysSerSerGlyGlyHisGluAsnSerHi 71
    |||||
Db 133 CGGTGGCGCGAGCTCAAGCGCCCTGTCTGCCCAAAATCGCGAGGTACTGAGAAAGCCCA 192
QY 71 sAsnSerValAspGluAlaLeuLeuLysAsGlySerGluGluValLeuPheTyrLe 91
    |||||
Db 193 CTATTCTGTGATGAGCTCTGTACTTAAGCAAAAGACGAGAGCTGCTCCCTTACCT 252
QY 91 uAnGlyArgCyaleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLy 111
    |||||
Db 253 GAATGACCGCTGTGTTTATCTAGTTGGAATGATGGTTCGCGCAAAACTACAGTTGGAA 312
QY 111 sIleMetSerGluValLeuGlyTyrSerPheAspSerAspLysLeuValGluGlnAl 131
    |||||
Db 313 GATAATAGCTGAAGTACTAGGCTATTCTTTGACAGTAAAGCTGGTTGAGCAGTC 372
QY 131 aValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAs 151
    |||||
Db 373 TGTGTGCATACCGTCGGTGGCTGAGATTTTTCAGTCCACAGTGAAGCATCTTTCAGAGA 432
QY 151 pAnGluSerSerValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGl 171
    |||||
Db 433 TAACGAGAGTGAGTACTAAGGGATTGTGTCATGTCACCGATTAAATTTGTTCCACAGG 492
QY 171 yGlyGlyAlaValIleArgProIleAsnTrpArgTyrMetLysArgGlyLeuSerValTr 191
    |||||
Db 493 AGGTGGTGGCGGTGATACGACCAATCAATTGGAGTATATGAAGAAGGATCTACTATTGG 552
QY 191 pLeuAspValProLeuAspAlaLeuAlaArgAlaIleAlaLysValGlyThrAlaSerAr 211
    |||||
Db 553 GTTAGATGTTCCATTGGACGCCCTTGCAGAAGAGATTGCTGCGGTGGTACTCGGTACG 612
QY 211 qProLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMe 231
    |||||
Db 613 ACCCTCTGTCATCAGGAATCTGGTGATCTTATGCAAGGCCCTATGCCAAACTTACAGC 672
QY 231 tLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluGl 251
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Db 673 ACTTTTGAACAAGAATGATTCATATGCTAATGCTGATGCCCGAGTTTCCCTTGAANA 732
QY 251 uIleAlaCysIleGlnGlyHisAspAspValSerLysLeuThrProThrAspIleAla 271
    |||||
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QY 271 eGluSerLeuHisLysIleGluSerPheValIleGlu 283
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Db 793 TGAGGCATTGCTAAAGATGGAGAGCTTTCTTACTGAG 829
RESULT 5
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LOCUS      Oryza sativa (japonica cultivar-group) chromosome 2 clone
DEFINITION      OJ1308_A10, *** SEQUENCING IN PROGRESS ***.
ACCESSION      AP004089
VERSION      AP004089.1 GI:15281368
KEYWORDS      HTG; HTGS PHASE2.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      1 Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE      Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
              clone:OJ1308_A10
JOURNAL      Published Only in Database (2001)
REFERENCE
AUTHORS      2 (bases 1 to 11177)
TITLE      Sasaki,T., Matsumoto,T. and Yamamoto,K.
JOURNAL      Direct Submission
COMMENT      Submitted (22-AUG-2001) Takuji Sasaki, National Institute of
              Agrobiological Resources, Rice Genome Research Program; Kamondai
              2-1-2, Tsukuba, Ibaraki 305-8602, Japan
              (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
              Tel:81-298-38-7441, Fax:81-298-38-7458)
              The nucleotide sequence of this BAC clone was generated by
              combining Monsanto and RGP-Japan sequencing data.
              NOTE: It currently consists of 1 contigs. Gaps between the contigs
              are represented as runs of N. The order of the pieces is believed
              to be correct as given, however the sizes of the gaps between them
              are based on estimates that have provided by the submitter. This
              sequence will be replaced by the finished sequence as soon as it is
              available and the accession number will be preserved.
              * NOTE: This is a 'working draft' sequence.
              * This sequence will be replaced
              * by the finished sequence as soon as it is available and
              * the accession number will be preserved.
FEATURES
  source      Location/Qualifiers
1. .111777     /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="genomic DNA"
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              /chromosomes="2"
              /clone="OJ1308_A10"
ORIGIN
Alignment Scores:
Pred. No.:    9,93e-52      Length:    111777
Score:        836.50       Matches:  263
Percent Similarity: 34.24%   Conservative: 14
Best Local Similarity: 32.51% Mismatches:  25
Query Match:  54.82%      Indels:    512
DB:           2           Gaps:     13
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QY 1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAlaAlaGlyPhe---GlySer 19
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Db 65897 ATGAGGCG---GGCGTGGGGCTGGCGTGCAGTCGCGGCGGGGGTTCGGCGGCTCC 65841
QY 20 SerArgHisArgGlyGlyLeu-----GlnAlaProThrGlySerLeuArg 34
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Db 65840 GACCGCGCGGAGCGCGCTCTACGCGCGGAGCGGCGCGGATCGGAGCTTGAGG 65781
QY 35 ValAlaAspProAlaGlyProAlaValAlaValArgAlaArgGlySerLysProValAla 54
    |||||
Db 65780 GTCGCTGAGCGCGGTGGCGAAGCCGCTGTGTGGGCTCGCGGGTCCAAGCGGCTGCC 65721
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Qy	55	ProLeuArgLeuArgAlaLysLysSerSerGly- CCG-----CTCCGTGCAAGAAATCGTCGG-AGGTACAGGGTCGCTGCCCTTCTCTCTT	65
Db	65720	CCG-----CTCCGTGCAAGAAATCGTCGG-AGGTACAGGGTCGCTGCCCTTCTCTCTT	65668
Qy	65	-----	65
Db	65667	CGTTCTGTCTCAGATTGGTTGATTGGCAAAAGTTTGTTGTTTTTGTGGACGAACTGGCG	65608
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Db	65607	GTCTGGCGCCATTGGGCCCTTTTTTTGTGTGTGTCGGATTTTTGTGTCGATCGGGATTTGTTG	65548
Qy	65	-----	65
Db	65547	ATAFTTGGAGGAAACACATGCAACGGGTGGTTGATTCCGTCACAAAAAAGCTT	65488
Qy	65	-----	65
Db	65487	GCAAGTAAGGAATTAGGTGTAAGGCTTCGAATGATCGAATACTGCAAAAGTTGT	65428
Qy	65	-----	65
Db	65427	GCCTCTTCTGTGTTTGCTTTTGCTATGGCGTCATTTTGGTTCAGATTTTGAGTCCTA	65368
Qy	65	-----	65
Db	65367	TTGTTCCGATTAGATTGATCAAAATCGATAGTTGATTCGGATTATTATTGGAAAGGTAG	65308
Qy	65	-----	65
Db	65307	GAAGAGATGAAGTTTCGCCCTATGATGGTCTTTCTAGATCAAGCCAATCTGAAAAATCC	65248
Qy	65	-----	65
Db	65247	ACGAGGTGTGATTATTATGTCTTCCAAATTCACAGAAATTGAGCTCTCCGTATTATTGT	65188
Qy	66	-----GlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLeuLys---81	
Db	65187	TCCTGTGCAGGTCAATGAACAATTGCATACTCGTTTGATGAAGCCCTCTTGTCTAAAGGTA	65128
Qy	81	-----	81
Db	65127	CTGCATAATCAAAATCAAAAGCGACACTGGAGTTTGCTTTTCTTCCATCATCTATGT	65068
Qy	82	-----ArgLysSerGluValLeuPheTyrLeuAsnGly93	
Db	65067	TCTAACCATCTGTTTATTTTTCAGAGAAATCAGAAAGTTCTCTCTATTTTGAATGGA	65008
Qy	94	ArgCysIleTyr-----97	
Db	65007	CGGTGTTATTACCTAGTTGGTTAGTTCTGAAACTTCTCATCTCCAAATATACGACT	64948
Qy	98	-----Leu98	
Db	64947	GAAAAAGATCAATATATAGATGGCATCTGAAATTCCTGGTTGATAAATAAAAACATGCTCTG	64888
Qy	99	ValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerCluValLeuGly118	
Db	64887	CA-GGAATGATGGGTCTCTGAAAAAGTACTGTGGGAAAGATCATGTCTGAAGTTTTGGGT	64829
Qy	119	Tyr-SerPhePheAspSer-----124	
Db	64828	TATTCTGTTCTTTTGTAGTAG-GTTTGTATTTTGTCTATTGTCACAGGAGATCTTGCCCTTGGT	64770
Qy	125	-----AspLysLeuValGlu129	
Db	64769	GCTCATGGTAATCTAAGCTTTTATTTCTGGAATTTGTTTTCAGTGATAAATTTGGTCGAA	64710
Qy	130	GlnAlaValGlyMetProSerValAlaGlnIlePheLysValHisSerClnAlaPhe149	
Db	64709	CAGCTGTGGCATGCCCTTCAGTCGTCAAATTTTCAAGGTTTCATAGTGAAGCCTTCTTT	64650
Qy	150	ArgAspAsnGlu-----153	

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Qy	153	-----	153
Db	64589	TAGCATTTGTTTACTTGTAGTTATCAGAAGGAAATCTGAGACTGATTATTTTCTCTGTG	64530
Qy	154	-----SerSerValLeuArgAspLeuSerSerMetArgArgLeu	166
Db	64529	GCTCTCTTTTATGCATTCACAGAGTAGTGTCTTGAGGGATTGTCTCAATGAAGCGATTA	64470
Qy	167	valvalalathrGlyGlyAlaValIleArgProIleAsnTrp	181
Db	64469	GTTGTTGCTACTGGAGGTGTGCTGTATTATCCAGCAGTTAACTGGTATCTGAGTTCAC	64410
Qy	181	-----	181
Db	64409	TCTATTTTTCCTGTTGGAAATAGTTATTTTGTGGCTTCTCTTATTTTGATTAAACAATATT	64350
Qy	182	-----ArgTyrMetLysArgGlyLeuSerValTrpLeuAs	193
Db	64349	GTGATCTCTTGTGTATTATCAGGAATACATGAAGAGGCCCTATCTGTTGGTTGGA	64290
Qy	193	pValProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLe	213
Db	64289	TGTGCCCTTGGACGCTCTTGCTAGCGCTATTGCTAAAGTGGGGACTGCCTCCGCTCTCT	64230
Qy	213	uLeuAspGlnProSerGlyAspProTyrAlaMetala	225
Db	64229	TCTAGATCAACCATCTGGTGATCCATACACATGGT-GACTACTTGGGCCCATGAATTTAT	64171
Qy	225	-----	225
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Qy	225	-----	225
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Qy	225	-----	225
Db	64050	AACTGCTAGTGTAATCTTTTCATTTTCAGTGTAATGAGTTGCTCACTGGATTTCTCT	63991
Qy	226	-----PheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAs	242
Db	63990	ATCTTAGGCTTTTCTAACTCAGCATGCTCGCGGAGCAAGGGCGATGCTTATGCAA	63931
Qy	242	nAlaAspValArgValSerLeuGlu	250
Db	63930	TGCTGATGTAGGGTTTCTTCTTGAAGGTATMACTTCACAAGTTTTCGAAAATCGCGCT	63871
Qy	250	-----	250
Db	63870	TTCCCATTTAGAAATATGTGCTAGGTATTGTGCGACACATTACTTTTAAAGTAATGCTTG	63811
Qy	251	-----GluIleAl	253
Db	63810	ATAACTCCAATTTTCCCTGCATAGAAATAACATATATGTTTTTGGAACTTGCAGAGATTGC	63751
Qy	253	aCysLysGlnGlyHisAspAspValSerLysLeuThrProThrAspIleAlaIleGluSe	273
Db	63750	ATCTAAACAGGGTCATGATGATGTATCGAAGCTAACACCACTGACATTGCTATTAGGCT	63691
Qy	273	rLeu	274
Db	63690	-ATGCAATGATAAGCTATTCTGAACCCCAATCAGGAGCAATATGAATCTTATTTTTTCT	63632
Qy	275	-----HisLysIle	277
Db	63631	AAGCTACTGAAACAATTTCCCTAAACAACATCTTGGCATTTTACAGTCGTTTCATAGAT	63572
Qy	277	eGluSerPheValIleGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSe	297

1898 TATTCGTTCTTTGATAG-GTTTGTATTTTGGCTATTGTCGAAGAGATCTTGCCCTTGGT 1956
125 - - - - -AspLysLeuValGlu 129
1957 GCTCATGGTAATCTAAGCTTTTATATTCTGGAATTGTTTGCAGTGTATAAATTTGGTCGA 2016
130 GluAlaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePhe 149
2017 CAAGCTGTGGGCATGCCCTTCAGTCGCTCAAATTTTCAAGGTTTCATAGTGAAGCTTCTTT 2076
150 ArgAspAsnGlu- - - - - 153
2077 AGGGAATAGGTAATCTTTTCTGAAATCCATCTTCTGCTAAACATGATCTACTATCT 2136
153 - - - - - 153
2137 TAGCAATTTGTTACTTGTAGTATATCAGAGGAAATCTGAGACTGATTATTTTCTCTGTG 2196
154 - - - - -SerSerValLeuArgAspLeuSerSerMetArgArgLeu 166
2197 GCTCTCTTTTATGCATTCACAGACTAGTGTCTTGAGGGAATTTGTCTCAATGAAGCGATTA 2256
167 ValValAlaThrGlyGlyAlaValIleArgProIleAsnTrp- - - - - 181
2257 GTTGTGCTACTGGAGGTGGTGTCTGTTATCCGACCAGTTAACTGGTATCTGGAGTTCACT 2316
181 - - - - - 181
2317 TCTATTTTCTGTTGGAATAGTTTATTTTGTGGCTTCTTATTTTGTATTAACAATATT 2376
182 - - - - -ArgTyrMetLysArgGlyLeuSerValTrpLeuAs 193
2377 GTGATCTCTTGTGTTATATCAGGAATACATGAAGAGGCTATCTGTTTGGTTGA 2436
193 pValProLeuAspAlaLeuAlaArgIleAlaLysValGlyThrAlaSerArgProLe 213
2437 TGTGGCCCTTGGAGCGCTCTGCTAGGCGTATTGCTAAAGTGGGACTGCCTCCGCTCTCT 2496
213 uLeuAspGlnProSerGlyAspProTyrAlaMetAla- - - - - 225
2497 TCTAGATCAACCATCTGTTGATCCATACACATAGGT-GACTACTGGCCCATGAATTTAT 2555
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2556 GCCATGCATCAATATGATATTATTTTCAGATGTATTTTAAATTTTAAATCAATCAATA 2615
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2616 TAGGCTCATTCATTCATAGTAAGTGAAGAACTGCAAGTATGATCCTGCACATCTGCAC 2675
225 - - - - - 225
2676 AACTGGTAGTGTAAATCTTTTCATTTTCAGTGTAGTATGAGTGTCTCACTGGATTTCTCT 2735
226 - - - - -PheSerLysLeuSerMetLeuAlaGlnArgGlyAspAlaTyrAlaAs 242
2736 ATCTTAGGCTTTTCTTAACTCAGCATGCTCGCGGAGCAAGGGGGGATGCTTATGCAA 2795
242 nAlaAspValArgValSerLeuGlu- - - - - 250
2796 TGCTGATGTGAGGTTTCTCTTGAAGGTATAACTTCACAAGTTTTCGCAAAATCCGCGCT 2855
250 - - - - - 250
2856 TTCCCAATTTAGAGATATGTGCTAGTATTATGTCGCGACATTAATTCTTTTAAGTAATGCTTG 2915
251 - - - - -GluIleAl 253
2916 ATAACTCCATTTTCTCCATAGATAACATATATGTTTTTGGAACTTGCAGAGATTGC 2975
253 aCysLysGlnGlyHisAspAspValSerLysLeuThrProThrAspIleAlaIleGluSe 273

Db 2976 ATCTAAACAGGGTCATGATGATGTATCGAAGCTAAACCACTGACATTTGCTATTGAGGT 3035
QY 273 rLeu- - - - - 274
Db 3036 -ATGCATGATAAGCTATTCTGAACCCACACATCAGGAGCAATATGAATCTTATTTTCTCT 3094
QY 275 - - - - -HisLysIle 277
3095 AAGTACTGAAACAATTTCCCTAAACAACATTTCTGGCATTTTACAGTCGTTTTCATAAGAT 3154
QY 277 eGluSerPheValIleGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSe 297
3155 CAGAACTTTGTTCATTTGAACATACCGTTGCAATCCGTTGGTGTGAGTCTCCAGGCTGACTC 3214
QY 297 rGlnIleGlnArgIleGlnThrLeu 305
Db 3215 ACGTGTCTCAGAGGATACAGACCTTG 3239
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LOCUS BAC clone:OSJNBa0078N1.
DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,
AP005848
ACCESSION AP005848.3 GI:46390919
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (24-OCT-2002) Takuji Sakaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannonnai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakia@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
On Apr 14, 2004 this sequence version replaced gi:33235585.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
(http://www.softberry.com/), GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://www.tigr.org/tdb/glimmer/glmr_form.html), RiceHMM
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The
genomic sequence was searched against NCBI NonRedundant Protein
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
sequence database at RGP or DBJ. Protein homologs of the coding
regions were searched against NCBI NonRedundant Protein database
with BLASTP. ESTs represent the identified cDNA sequences using
BLASTN with the corresponding DBJ accession no. and RGP clone ID.
Full-length cDNAs represent the identified cDNA sequences using
BLASTN with the corresponding DBJ accession no.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without
significant homology to any protein but with full-length cDNA or
EST homology (covering almost the entire length of partial
sequence) is classified as an 'unknown' protein. A gene predicted
by two or more gene prediction programs is classified as a
'hypothetical' protein according to IRGSP standard. A gene
predicted by a single gene prediction program is also classified as
a probable 'hypothetical' protein and is included as a
miscellaneous feature of the sequence.

The orientation of the sequence is from M13rev to -21M13 of the BAC clone. This sequence of OSJNBa0078N11.6 clone has an overlap with OSJNBb0024K03 (DDBJ: AP005733) clone at 5' end and with F0431B06 (DDBJ: AP004774) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/GenomeSeq.html>.

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Score:	836.50	Matches:	263
Percent Similarity:	34.24%	Conservative:	14
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Query Match:	54.82%	Indels:	512
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Db	145666	ATGGAGGCG---GGCGTGGGCTGGGCTGCAGTCGGCGGGGGTTCGGCGGCTCC	145722
QY	20	SerArgHisArgGlyGlyLeu-----GlnAlaProThrGlySerLeuArg	34
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QY	35	ValAlaAspProAlaGlyProAlaValAlaValAlaValArgAlaArgGlySerLysProValAla	54
Db	145783	GTCGCTGAGCGCGGGTGGCGAAGCGGCTGTGTGGGCTCGCGGTCCTCAAGCGGTCGCC	145842
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QY	65	-----	65
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Db	145956	GTCTGGCGCCATTGGGCCCTTTTTTTGTGTGTCCGATTTTGTCTGATCGGAGTTGTG	146015
QY	65	-----	65
Db	146016	ATATTTGGAGGAACACATGGAACGGGTGCGTTGATTTCGGTCAAAAAAAGAGCTT	146075
QY	65	-----	65
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Db	146136	GCCTCTTCTGTGTTGTCTTTTGTCTATGCGGTCCATTTTGGTTTCAGATTTTCAGTCCTA	146195
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QY	65	-----	65
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QY	66	-----GlyHisGlnAsnSerHisAsnSerValAspGluAlaLeuLeuLys---	81
Db	146376	TCCTGTGCAGGTCAATGAACAATTGCATACTACCTCGTTGATGAAGCCCTCTTGTCAAAGGTA	146435
QY	81	-----	81
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QY	82	-----ArgLysSerGluGluValLeuPheTyrLeuAsnGly	93
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QY	94	ArgCysIleTyr-----	97
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QY	98	-----Leu 98	
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QY	99	ValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGly	118
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QY	125	-----AspLysLeuValGlu 129	
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QY	150	ArgAspAsnGlu-----	153
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QY	154	-----SerSerValLeuArgAspLeuSerSerMetArgArgLeu 166	
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QY	193	pValProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLe	213
Db	147274	TGTGCCCTTGGACGCTCTTGTCTAGGCGTATTGCTAAAGTGGGAGCTGCCCTCCGCTCTCT	147333
QY	213	uLeuAspGlnProSerGlyAspProTyrAlaMetAla-----	225
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Db	147393	GCCATGCATGAATATGATATTATTTTCAGATGTATTTTAAAAATTTTAAATCAGTCAATA	147452
QY	225	-----	225
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QY	226	-----PheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyAlaAs 242	
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QY	251	-----GluIleAl	253
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QY	273	rIeu-----	274
Db	147873	-ATGCATGATAAGCTATTCTGAACCCACAATCAGGAGCAATATGAATCTTATTTTCT	147931
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QY	277	eGluSerPheValIleGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSe	297
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DEFINITION	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6, PAC clone:P0690H04.		
ACCESSION	AP003513		
VERSION	AP003513.2	GI:42415338	
KEYWORDS	Oryza sativa (japonica cultivar-group)		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.		
REFERENCE	1		
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.		
TITLE	Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0690H04		
REFERENCE	2 (bases 1 to 137319)		
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.		
JOURNAL	Direct Submission		
AUTHORS	Submitted (11-APR-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan		
JOURNAL	[E-mail:tsasak@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468]		
COMMENT	On Feb 5, 2004 this sequence version replaced gi:13603473. Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4 (http://globin.cse.psu.edu/html/docs/sim4.html), gap2 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI Nonredundant protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using		

BLASTN with the corresponding DDBJ accession no.	
A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.	
The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0690H04 clone has an overlap with P0639H11 clone (DDBJ: AP005545) at 5' end and an overlap with P0425F05 (DDBJ: AP003569) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html .	
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QY 296 GluSerGlnIleGlnArgIleGlnThrLeu 305
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LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:J013123P09, full
DEFINITION insert sequence.
ACCESSION AK067948
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AK067948.1 GI:32977966
FLJ_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Euryza sativa (japonica cultivar-group)
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team.;
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Ootomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN.;
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
22752273
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2 (bases 1 to 2127)
Adjimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Doi,K.,
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kurohara,C., Kusumegi,T., Kusumegi,T., Li,C., Lu,M.,
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K.,
Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H.,
Osato,N., Ota,Y., Ootomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toda,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.
Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
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305-8602, Japan [E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007]
This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
```

and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirotsuka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oeato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tgami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES

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ORIGIN

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US-10-660-226-10 (1-305) x AK067948 (1-2127)

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VERSION			
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TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			

Masuda, H., Matsuura, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaka, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, F., Tomaru, A., Toyota, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

TITLE

JOURNAL

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@ias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)

COMMENT This clone is one of the 28K full-length cDNA clones from japonica rice.

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.
 FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Iu, M., Masuda, H., Miura, J., Mizuno, K., Nariikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsuura, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaka, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyota, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES

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US-10-660-226-10 (1-305) x AK070318 (1-1167)

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 ACCESSION
 AKI18899
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 KEYWORDS
 FLI CDNA; CAP trapper.
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 Arabidopsis thaliana (thale cress)
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 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1
 Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
 TITLE
 Arabidopsis thaliana full-length cDNA
 JOURNAL
 Published Only in Database (2002)
 REFERENCE
 2 (bases 1 to 1300)
 Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J.,

KEYWORDS SOURCE ORGANISM

FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 903)

REFERENCE AUTHORS

Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P.,
Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
Ecker, J.R.

TITLE JOURNAL REFERENCE AUTHORS

Unpublished
2 (bases 1 to 903)
Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P.,
Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
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Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
Ecker, J.R.

TITLE JOURNAL

Direct Submission
Submitted (14-MAR-2003) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGECC (SSP) Consortium members constructed and
sequenced the pUNI (ORF) clones using the RAFL cDNAs: Kim, C.J.,
Chen, H., Cheuk, R., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M.,
Dale, J.M., Hsuan, V.W., Jones, T., Karlin-Neumann, G., Lam, B.,
Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J.,
Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,
Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A., and
Ecker, J.R.

Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
contributed equally to this work as PIs.

FEATURES source

Location/Qualifiers
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ORIGIN

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Query Match:	39.74%	Indels:	9
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RESULT 15

AK117791

LOCUS

DEFINITION

complete cds, clone: RAFL17-48-C24.

AK117791

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1

Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J.,

Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P.,

PLN 14-FEB-2004

linear

putative shikimate kinase,

RAFL17-48-C24.

GI:26450650

FLI CDNA; CAP trapper.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

TITLE
JOURNAL
REFERENCE
AUTHORS
Kawai,J., Hayashizaki, Y. and Shinozaki, K.
Arabidopsis thaliana full-length cDNA
Published Only in Database (2002)
2 (bases 1 to 1294)
Seki,M., Iida,K., Satou,M., Sakurai,T., Akiyama,K., Ishida,J.,
Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Carninci,P.,
Kawai,J., Hayashizaki, Y. and Shinozaki, K.
Direct Submission
Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences
Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
230-0045, Japan [E-mail:msseki@gsc.riken.go.jp,
URL:http://pfweb.gsc.riken.go.jp, Tel:81-45-503-9625,
Fax:81-45-503-9586]
COMMENT
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al. (1998) Plant J. 15:707-720;
Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et
al. (2001) Genomics 77:79-90) digested with BamHI and SalI.
This clone is in a modified pBluescript vector.
Please visit our web site (http://pfweb.gsc.riken.go.jp/) for
further details.

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ORIGIN

Alignment Scores:
Pred. No.: 1.26e-36 Length: 1294
Score: 606.50 Matches: 130
Percent Similarity: 71.37% Conservative: 37
Best Local Similarity: 55.56% Mismatches: 58
Query Match: 39.74% Indels: 9
DB: 8 Gaps: 5

US-10-660-226-10 (1-305) x AK117791 (1-1294)

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QY 71 HisAsnSerValAsp--GluAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuPhe 89
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DB 510 TATTTAAATGGACGATCGATGATCTTGTGGTATCATGGTTCGGGAAACGACTGTA 569
QY 110 GlyLysIleMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGlu 129
DB 570 GGGAAGATTATGGCAAGATCGCTTGTGTTATACATTTCTTGTGACACTTTGTATCGAG 629
QY 130 GlnAlaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePhe 149

DB 630 CAGGCTATGAAGGGAACCTTCTGTAGCTCAGATATTTGAGCATTTTCGGTGAGAGTCTCTTC 689
QY 150 ArgAspAsnGluSerSerValLeuArgAspLeuSerSerMet---ArgArgLeuValVal 168
DB 690 AGAGAAAAAGAGACTGAAGCGTTAAAGAACTCTCTTTGATGTATACCACCAAGTTGTGTT 749
QY 169 AlaThrGlyGlyGlyAlaValIleArgProIleAsnTTPArgTyrMetLysArgGlyLeu 188
DB 750 TCAACCGGGGGGCGGCGAGTTATAGACCCATCAATTGGAAGTACATCATATAAAGTATT 809
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Search completed: August 25, 2005, 22:17:38
Job time : 5030 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 25, 2005, 17:38:27 ; Search time 610 Seconds

(without alignments)
2959,871 Million cell updates/sec

Title: US-10-660-226-10

Perfect score: 1526

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Fgapop 6.0 , Fgapext 7.0
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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	656	43.0	1363	3 AAC36026	Aac36026 Arabidops
3	650	42.6	1365	3 AAC50026	Aac50026 Arabidops
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5	631.5	41.4	637	10 ADK52674	Adk52674 Plant DNA

6	626.5	41.1	1484	3 AAC40184	Aac40184 Arabidops
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10	473	31.0	1010	13 ADR60835	Adr60835 Cotton CD
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13	368	24.1	329	10 ADK58255	Adk58255 Plant DNA
14	362.5	23.8	614	13 ADR60836	Adr60836 Cotton CD
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16	318.5	20.9	570	13 ADS47877	Ads47877 Bacterial
17	315	20.6	564	13 ADT45202	Adt45202 Bacterial
18	307	20.1	528	13 ADT46243	Adt46243 Bacterial
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20	271.5	17.8	537	10 ADK58256	Adk58256 Plant DNA
21	256	16.8	226	7 ADK67657	Adk67657 Corn seed
22	254	16.6	5330	2 AAX84337	Aax84337 Stealth v
23	252	16.5	582	13 ADT45821	Adt45821 Bacterial
24	249.5	16.3	507	13 ADS45422	Ads45422 Bacterial
25	245	16.1	696	12 ADL02481	Adl02481 DNA encod
26	245	16.1	14335	4 AAF28524	Aaf28524 Genomic f
27	241	15.8	678	12 ADM34080	Adm34080 Cryptospo
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31	228.5	15.0	504	13 ADS56012	Ads56012 Bacterial
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33	226.5	14.8	480	10 ADE82174	Ade82174 Arabidops
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35	222	14.5	603	9 ADA30736	Ada30736 DNA encod
36	222	14.5	603	11 ACH97846	Ach97846 Klebsiell
37	220	14.4	438	13 ADT46957	Adt46957 Bacterial
38	220	14.4	444	13 ADT43049	Adt43049 Bacterial
39	218	14.3	513	10 ABZ38655	Abz38655 N. gonorr
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42	218	14.3	349980	3 AAF21612	Aaf21612 Neisseria
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ALIGNMENTS

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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 63305.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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Length: 1363
Percent Similarity: 79.80%
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Best Local Similarity: 62.56%
Conservative: 35
Query Match: 42.99%
Mismatches: 41
Indels: 0
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Gaps: 0

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Db 368 ATTCTCAAGAGAAAGCAGAGAGGTTAAACCGTATTTGATGGAGATCTATGTACCTT 427
QY 99 ValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGly 118
Db 428 GTCGGAATGATGGTTCTGGGAAACCACTGTGGGAAAGTTAATGTCCAAAGTGTCTCGGT 487
QY 119 TyrSerPhePheAspSerAspLysLeuValGluAlaValGlyMetProSerValAla 138
Db 488 TATACGTTCTTTCACCTCGCAGCATTGATTGAACAGCGCATGAATGGAACCTTCTGTGCA 547
QY 139 GluIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArg 158
Db 548 GAGATATTTGTTTCATCAGGAGAGAAATTTTTAGAGGAAGGAGACCGATGCGCTTAAG 607
QY 159 AspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyAlaValIleArgPro 178
Db 608 AAGCTCTCTTCGAGGTATCAAGTTGTTTTCACAGGTGGAGTGCAGTTATAAGACCC 667
QY 179 IleAsnTyrArgTyrMetLysArgGlyLeuSerValTyrLeuAspValProLeuAspAla 198
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QY 199 LeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSer 218
Db 728 TTAGCCCATAGATCCTGCTGTGTGAACATGATTCAGACCATGCTACAGCATGAATCA 787
QY 219 GlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnArgGlyAsp 238
Db 788 GGAGATGCTACTCAGTGGCTTTCAAACGCTCTCTCGCTATTTGGGACGACGCGGTGAA 847
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QY 259 AspAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGlu 278
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RESULT 3
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XX
DT 18-OCT-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
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PR 17-AUG-1999;	99US-0149175P.	Db 438 ATGATGGGTTCTGGGAAACAACTGTGGGAAAGTTAATGTCCAAAAGTGTCTCGTTATACG 497	
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PR 06-OCT-1999;	99US-0157865P.		
PR 07-OCT-1999;	99US-0158029P.		

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PR 16-AUG-1999;	99US-0149368P.	PR 17-AUG-1999;	99US-0149175P.	Db 552	CAAGAAAGCAGAGAGGTTAAACCGTATTGATGGACGATCTATGTACCTTGTCCGA 611
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PR 23-AUG-1999;	99US-0149802P.	PR 25-AUG-1999;	99US-0150366P.	Db 672	TTCTTTGATCGGACACTTTGATTGAACAGCGGATGAATGGAACTTCTGTTCACAGATA 731
PR 25-AUG-1999;	99US-0150366P.	PR 26-AUG-1999;	99US-0150884P.	Qy 141	PheLysValHisSerGluAlaPhePheArgAspAenGluSerSerValLeuArgAspLeu 160
PR 26-AUG-1999;	99US-0150884P.	PR 27-AUG-1999;	99US-0151065P.	Db 732	TTTGTTCATCAGGAGAGAAATTTTTTAGAGAAAGGAGACCGATCGCTTAAGAAGCTC 791
PR 27-AUG-1999;	99US-0151065P.	PR 30-AUG-1999;	99US-0151303P.	Qy 161	SerSerMetArgArgLeuValValAlaThrGlyGlyAlaValAlaIleArgProIleAen 180
PR 30-AUG-1999;	99US-0151303P.	PR 31-AUG-1999;	99US-0151438P.	Db 792	TCTTCGAGGTATCAAAGTTGTTTCCACAGGTGGAGGTGCAGTTTATAAGACCCATTAC 851
PR 01-SEP-1999;	99US-0151930P.	PR 07-SEP-1999;	99US-0152363P.	Qy 181	TtpArgTyrMetLysArgGlyLeuSerValTtpLeuAspValProLeuAspAlaLeuAla 200
PR 07-SEP-1999;	99US-0152363P.	PR 10-SEP-1999;	99US-0153070P.	Db 852	TGGAAGTATATGCATAAAGGAATCAGCATTTGGCTAGATGTGCCTCTAGAAGCATTAGCC 911
PR 13-SEP-1999;	99US-0153758P.	PR 15-SEP-1999;	99US-0153758P.	Qy 201	ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220
PR 15-SEP-1999;	99US-0153758P.	PR 16-SEP-1999;	99US-0154018P.	Db 912	CATAGATCGCTGCTGTGGAACTGATTCACGACCACTGCTACAGATCAATCAGAGAT 971
PR 16-SEP-1999;	99US-0154018P.	PR 20-SEP-1999;	99US-0154779P.	Qy 221	ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyr 240
PR 20-SEP-1999;	99US-0154779P.	PR 23-SEP-1999;	99US-0155486P.	Db 972	GCATACTCAGTGGCTTCAAACGTCTCTCGGCTATTGGGACGACGCGGTGAAGCATAC 1031
PR 23-SEP-1999;	99US-0155486P.	PR 24-SEP-1999;	99US-0155659P.	Qy 241	AlaAenAlaAspValArgValSerLeuGluIleAlaCysLysGlnGlyHisAspAsp 260
PR 24-SEP-1999;	99US-0155659P.	PR 28-SEP-1999;	99US-0156458P.	Db 1032	ACAAACGCCAAATGCCAGAGTCTCTTAGAAAATATTGCAGCAAGCGGTGATATAAAT 1091
PR 28-SEP-1999;	99US-0156458P.	PR 29-SEP-1999;	99US-0156596P.	Qy 261	ValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGluSerPhe 280
PR 04-OCT-1999;	99US-0157117P.	PR 05-OCT-1999;	99US-0157753P.	Db 1092	GTCTCAGATCTCACACCACTGAATTTGCTATCGAGGCTTCGACGAAGTTCTGAGCTTT 1151
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PR 12-OCT-1999;	99US-0158369P.	PR 13-OCT-1999;	99US-0159293P.	ADK52674	
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PR 14-OCT-1999;	99US-0159330P.	PR 14-OCT-1999;	99US-0159331P.	XX	ADK52674;
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PR 18-OCT-1999;	99US-0159638P.	PR 21-OCT-1999;	99US-0160741P.	DE	Plant DNA sequence which confers altered metabolic characteristic #57.
PR 21-OCT-1999;	99US-0160767P.	PR 21-OCT-1999;	99US-0160768P.	XX	altered metabolic characteristic; plant; acid metabolism;
PR 21-OCT-1999;	99US-0160770P.	PR 21-OCT-1999;	99US-0160814P.	XX	alcohol metabolism; fatty acid metabolism;
PR 21-OCT-1999;	99US-0160815P.	PR 22-OCT-1999;	99US-0160980P.	XX	branched fatty acid metabolism; alkaloid metabolism;
PR 22-OCT-1999;	99US-0160981P.	PR 25-OCT-1999;	99US-0161405P.	XX	amino acid metabolism; ester metabolism; glyceride metabolism;
PR 25-OCT-1999;	99US-0161404P.	PR 25-OCT-1999;	99US-0161406P.	XX	phenolic metabolism; carbonyl metabolism; steroid metabolism;
PR 25-OCT-1999;	99US-0161406P.	PR 26-OCT-1999;	99US-0161359P.	XX	terpene metabolism; isoprenoid metabolism; alkene metabolism;
PR 26-OCT-1999;	99US-0161360P.	PR 26-OCT-1999;	99US-0161361P.	XX	alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
PR 28-OCT-1999;	99US-0161920P.	PR 28-OCT-1999;	99US-0161922P.	XX	quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
PR 28-OCT-1999;	99US-0161923P.	PR 29-OCT-1999;	99US-0162142P.	XX	Nicotiana benthamiana.
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		Score:	80.10%	Conservative:	35
		Percent Similarity:			

PD 13-MAR-2003.
 XX
 PP 30-AUG-2002; 2002WO-US027884.
 XX
 PR 31-AUG-2001; 2001US-0316471P.
 XX
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 XX
 PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
 PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
 XX WPI; 2003-313091/30.
 XX
 XX Novel genes that confer altered metabolic characteristics in Nicotiana
 PT benthamiana plants, useful for altering the levels of metabolites e.g.
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
 XX
 PS Claim 1; SEQ ID NO 57; 2576pp; English.
 XX
 CC The invention comprises DNA sequences which confer an altered metabolic
 CC characteristic when they are expressed in a plant. The DNA sequences of
 CC the invention are useful for producing plants with an altered metabolic
 CC characteristic, such as: altered acid metabolism, alcohol metabolism,
 CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
 CC base metabolism, altered amino acid metabolism, altered ester metabolism,
 CC altered glyceride metabolism, altered phenolic metabolism, altered
 CC carbohydrate metabolism, altered sterol, oxygenated terpene, or
 CC isoprenoid metabolism, alkene or alkene metabolism, hydrocarbon
 CC metabolism, ketone or quinone metabolism. The DNA sequences of the
 CC invention may be used to provide disease resistance in a plant and gene
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a
 CC DNA sequence of the invention.
 XX
 SQ Sequence 637 BP; 185 A; 103 C; 165 G; 184 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9,42e-52 Length: 637
 Score: 631.50 Matches: 121
 Percent Similarity: 80.73% Conservative: 34
 Best Local Similarity: 63.02% Mismatches: 36
 Query Match: 41.38% Indels: 1
 DB: 10 Gaps: 1

US-10-660-226-10 (1-305) x ADK52674 (1-637)

QY 90 TyrLeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrVal 109
 Db 9 TATCTAGATGGACGATGTATATACCTCGTGGAGTATCGCTCGCAAAAACACTGTG 68
 QY 110 GlyLysIleMetSerGluValLeuGlyTyrSerPheAspSerAspLysLeuValGlu 129
 Db 69 GCGCGTATTGGCAGAAACACTGGGATATCTCTTTTGACTGTGACAGGCTGATAGAG 128
 QY 130 GlnAlaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePhe 149
 Db 129 CAGCGCTGTTGGTGAACACTACAGTAGCTGAATCTTCAAGCTTCGTGGAGAGAGCTTCTTT 188
 QY 150 ArgAspAsnGluSerSerValLeuArgAspLeuSerSerMetMetArgLeuValAla 169
 Db 189 AGGGACAATGAGACGAGGAGGTATTGCACAAAGCTGTCTGCGATGCAATCGGCTTGTTC 248
 QY 170 ThrGlyGlyGlyAlaValIleArgProIleAsnTyrArgTyrMetLysArgGlyLeuSer 189
 Db 249 ACAGGTGGAGGTGCAGTTGTCTGCCATTAATTGGACATATGACCAAGGGTATTAGT 308
 QY 190 ValTrpLeuAspValProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAla 209
 Db 309 GTTTGGTGTAGATGCTCTTTAGATGCTTTGGCCAAGAGAGTTACTCTCTGAAGAACTAAA 368
 QY 210 SerArgProLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeu 229
 Db 369 TCTCGACCCCTATTACATGAAGAATCAGGAGACATTTATGATAAGACTTTGAAGCGGTTA 428

QY 230 SerMetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeu 249
 Db 429 ACTACTTTTAATGGAGACAAGGGTGAATACTATGCCAATGCAAGTGTCAAGGTTTCACCTA 488
 QY 250 GluGluIleAlaCysLysGlnGlyHisAspAspValSerLysLeuThrProThrAspIle 269
 Db 489 GAAATATATTGCAGTGAAGAGGGA---AAAGATGCTGCCATATTACACCTACTGAAT 545
 QY 270 AlaIleGluSerLeuHisLysIleGluSerPheVal 281
 Db 546 ACTTAGAGGTCTTATATCAAAATTCAGAACTTCTTCTTA 581
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 ID AAC40184 standard; DNA; 1484 BP.
 XX AAC40184;
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 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 27368.
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 KW Hybridization assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic pathway;
 KW promoter; termination sequence; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 FN EF1033405-A2.
 XX
 PD 06-SEP-2000.
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 PF 25-FEB-2000; 2000EP-00301439.
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PR 10-SEP-1999; 99US-0153070P.
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PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.:
Score:

8.93e-51
626.50

Length:
Matches:

1484
126

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Percent Similarity: 79.31% Conservative: 35
Best Local Similarity: 62.07% Mismatches: 42
Query Match: 41.06% Indels: 1
DB: 3 Gaps: 0

US-10-660-226-10 (1-305) x AAC40184 (1-1484)

QY 79 LeuLeuLysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCysLeuTyrLeu 98
Db 539 ATTCTCAAGAGAAACAGAGAGGTTAAACCGTATTGAATGGACGATCTATGTACCTT 598
QY 99 ValGlyMetMetClySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGly 118
Db 599 GTCGGAATGATGGTTCTCGGAAACCACTGTGGAAAGTTAATGTCCAAGTGTCTCGGT 658
QY 119 TyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAla 138
Db 659 TATACGTTCTTGACATCGACACTTGTGATGAGG--GCATGATGAATGAACTTCTGTGCA 716
QY 139 GlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGlnSerSerValLeuArg 158
Db 717 GAGATATTGTTTCATCAGCAGAGAGAAATTTTTAGAGGAAAGGAGACCGATCGCTTAAG 776
QY 159 AspLeuSerSerMetArgArgLeuValAlaThrGlyClyValAlaValIleArgPro 178
Db 777 AAGCTCTCTTCGAGGATCAAGTTGTGTTCACAGGTGGAGGTGCAGTTATAAGACCC 836
QY 179 IleAsnTrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAla 198
Db 837 ATTAACCTGGAAATGATATGATAAAGGAATCAGCATTTGGCTAGATGTGCTCTAGAGCA 896
QY 199 LeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSer 218
Db 897 TTAGCCCATAGAATCGCTGCTGTGTGAACATGATTACAGACCACTGCTACACGATGAATCA 956
QY 219 GlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAsp 238
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QY 239 AlaTyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHis 258
Db 1017 GCATACACAAACCAATCCAGAGTCTCTTAGAAAAATTTGACAAAGCGTGGCTAT 1076
QY 259 AspAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGlu 278
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QY 279 SerPheVal 281
Db 1137 AGCTTTCTA 1145

RESULT 7
ID AAC47100 standard; DNA; 1095 BP.
AC AAC47100;
AC AAC47100;
DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 52566.
DE Arabidopsis thaliana.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX PN
XX XX
XX 06-SEP-2000.
XX XX
XX 25-FEB-2000; 2000EP-00301439.
XX XX
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PR	16-JUL-1999;	99US-0144086P.
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PR	05-AUG-1999;	99US-0147260P.
PR	06-AUG-1999;	99US-0147303P.
PR	06-AUG-1999;	99US-0147416P.
PR	09-AUG-1999;	99US-0147493P.
PR	09-AUG-1999;	99US-0147935P.
PR	10-AUG-1999;	99US-0148171P.
PR	11-AUG-1999;	99US-0148319P.
PR	12-AUG-1999;	99US-0148341P.
PR	13-AUG-1999;	99US-0148565P.
PR	13-AUG-1999;	99US-0148684P.
PR	16-AUG-1999;	99US-0149368P.
PR	17-AUG-1999;	99US-0149175P.
PR	18-AUG-1999;	99US-0149426P.
PR	20-AUG-1999;	99US-0149722P.
PR	20-AUG-1999;	99US-0149723P.
PR	20-AUG-1999;	99US-0149929P.
PR	23-AUG-1999;	99US-0149902P.
PR	23-AUG-1999;	99US-0149930P.
PR	25-AUG-1999;	99US-0150566P.
PR	26-AUG-1999;	99US-0150884P.
PR	27-AUG-1999;	99US-0151065P.
PR	27-AUG-1999;	99US-0151066P.
PR	27-AUG-1999;	99US-0151080P.
PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.

PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
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PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

US-10-660-226-10 (1-305) x AAC47100 (1-1095)

QY

57

ArgLeuArgAla-----LysLysSerSerGlyGlyHisGluAsnSer-----

70

Db

209

CGACTTAGATCAGTTTCTGATAAGAACTCCTCAGCATTTGTTGGAACCTGGAAGTCTTCTT

268

QY

71

HisAsnSerValAspGlu-----AlaLeuLeuLeuLysArgLysSerGluGluValLeu

88

Db

269

CATTCTCCATTTGATGAAGAACACAGATTTTGAAGCAGAAAAAGCTGAGAGGTTAA

328

QY

89

PheTyrLeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThr

108

Db

329

CCGTATTAAATGGACGATCGATGATCTTTGTTGATGATGGTTCGGGAAAACGACT

388

QY

109

ValGlyLysIleMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuVal

128

Db

389

GTAGGGAAGATTATGGCAAGATCGCTTGGTTATACATTTCTTTGATTTGTGCACATTTGATC

448

QY

129

GluGlnAlaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhe

148

Db

449

GAGCAGGCTTATGAAGGAACTTCTGTAGCTGAGATATTTGACATTTCCGTGAGAGTGT

508

QY

149

PheArgAspAsnGluSerSerValLeuArgAspLeuSerSerMet---ArgArgLeuVal

167

Db

509

TTTACAGAAAAAGAGACTGAACGGTTAAAGAACTCTCTTTGATGTACCACCAAGTTGTT

568

QY

168

ValAlaThrGlyGlyAlaValIleArgProIleAsnTyrArgTyrMetLysArgGly

187

Db

569

GTTCACCGGGGGGGGCGAGTTATAGACCCATCAATTGGAAGTACATGCATAAAGT

628

KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

XX Arabidopsis thaliana.
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
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XX 21-APR-1999; 99US-0130449P.
XX 23-APR-1999; 99US-0130510P.
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XX 04-MAY-1999; 99US-0132484P.
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XX 06-MAY-1999; 99US-0132486P.
XX 07-MAY-1999; 99US-0132487P.
XX 11-MAY-1999; 99US-0132863P.
XX 14-MAY-1999; 99US-0134218P.
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XX 14-MAY-1999; 99US-0134221P.
XX 14-MAY-1999; 99US-0134370P.
XX 18-MAY-1999; 99US-0134768P.
XX 19-MAY-1999; 99US-0134941P.
XX 20-MAY-1999; 99US-0135124P.
XX 21-MAY-1999; 99US-0135353P.
XX 24-MAY-1999; 99US-0135629P.
XX 25-MAY-1999; 99US-0136021P.
XX 27-MAY-1999; 99US-0136392P.
XX 28-MAY-1999; 99US-0136782P.
XX 01-JUN-1999; 99US-0137222P.
XX 03-JUN-1999; 99US-0137528P.
XX 04-JUN-1999; 99US-0137502P.
XX 07-JUN-1999; 99US-0137724P.
XX 08-JUN-1999; 99US-0138094P.
XX 10-JUN-1999; 99US-0138540P.
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XX 18-JUN-1999; 99US-0139458P.
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XX 18-JUN-1999; 99US-0139750P.
XX 18-JUN-1999; 99US-0139763P.
XX 21-JUN-1999; 99US-0139817P.
XX 22-JUN-1999; 99US-0139899P.
XX 23-JUN-1999; 99US-0140353P.
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PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
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PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
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PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
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PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
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PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.

CC with the property, and growing the transformed plant. The polypeptide is
 CC useful for improving plant cold tolerance, manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, improving plant
 CC drought tolerance, providing increased resistance to plant disease,
 CC producing galactanman (or lignin or plant growth regulators), improving
 CC plant heat tolerance, improving plant tolerance to herbicides, increasing
 CC the rate of homologous recombination in plants, improving plant tolerance
 CC to extreme osmotic conditions or to pathogens or pests, improving yield
 CC by modification of photosynthesis, modifying seed oil or protein yield
 CC and/or content, improving yield by modification of carbohydrate, nitrogen
 CC or phosphorus use and/or uptake, or improving yield by providing improved
 CC plant growth and development under at least one stress condition. The
 CC polynucleotide and polypeptide may also be used in recombinant DNA
 CC constructs, in physical arrays of molecules, as plant breeding markers,
 CC or in computer-based storage and analysis systems. The present sequence
 CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20040181830. However only 6585
 CC polynucleotide sequences were available, the remaining 5213
 CC polynucleotides and all 58798 protein sequences were not present.
 XX
 SQ Sequence 1010 BP; 286 A; 180 C; 234 G; 310 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,976-36 Length: 1010
 Score: 473.00 Matches: 121
 Percent Similarity: 59.53% Conservative: 32
 Best Local Similarity: 47.08% Mismatches: 61
 Query Match: 31.00% Indels: 45
 DB: 13 Gaps: 5

US-10-660-226-10 (1-305) x ADR60835 (1-1010)

QY 30 ThrGlySerLeuArgValAlaAapProAlaGlyProAlaValAlaValArgGly 49
 DB 214 ACTGGTCTCTTGGGTTCTC-----GATCGGATAGCAAGCAACAAAG 258
 QY 50 SerLysProValAlaProLeuArgLeuArgAlaLysLysSerSerGlyGlyHisGlu--- 68
 DB 259 ACCCGGGTGTGTTTTCGGCCCACTTTCGGTTTCAGACATCTTCCAATGACATAGATCA 318
 QY 68 ----- 68
 DB 319 GTCTCTTTGGAGGTTTCTGCTCTCTATACGAACCTTTTCAGCTTCAACAATGGAACCT 378
 QY 69 ---AsnSerHisAsnSerValAspGluAlaLeuLeuLeuLysArgLysSerGluGluVal 87
 DB 379 GGCAGCATTCATGCACCTTTTGGTGAAGCTTTTAATGTTAAAGAAATAAGTCACTAGAGTT 438
 QY 88 LeuPheTyLeuAsnGlyArgCysIleTyLeuValGlyMetMetGlySerGlyLysSer 107
 DB 439 GAGCCATATTAATGGGCACAGTATATATCTTTGGATGTAAGGCTCTGGAACCT- 497
 QY 108 ThrValGlyLysIleMetSerGluValLeuGlyTyTyrSerPhePheAspSerAspLysLeu 127
 DB 498 ACAGTGGCAAAATCTCTCCCATGTACTCGGTTATTCATT-----TGTGACAGGTTG 551
 QY 128 -ValGluGluAlaValGlyMetPro----- 135
 DB 552 AATATTAGAGTGTATTCTCTCTGATGTCTACCAATTTCAAGAGAGTGTAATGGAAT 611
 QY 136 -SerValAlaGluIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSe 155
 DB 612 GTCTGTAGCTGGAATATTTAAGCTTCTATGGGAGAGTTCTTCAGAAAAAAGAGACTGA 671
 QY 155 rValLeuArgAspLysSerSerMetArgLeuValValAlaThrGlyGlyAlaVal 175
 DB 672 GGTATTGCAGGCTTCTTCACAGAAACAACCTTGTGTCTACTGGCGAGGTGCAGT 731
 QY 175 lIleArgProIleAsnTrpArgTyrMet----LysArgGlyLeuSerValTrpLeuAspVa 194
 DB 732 TGTACAGGATGTGAACCTGGGACTATATGCAGAGAAGGGGATGTTGTCTGTGTAGATGT 791

QY 194 lProLeuAspAlaLeuAlaAaArgIleAlaLysValGlyThrAlaSerArgProLeuLe 214
 DB 792 ACCTTTGGAGCCTTGGCACAAGGATGTCAGTAGTACTCATTTCTCGTCCCTTTT 851
 QY 214 uAspGlnProSerGlyAspProTyAlaMetAlaPheSerLysLeuSerMetLeuAlaGl 234
 DB 852 GCATTATGAAGATGCGGATCCATATACAAAGGCTTA-AAACGCTCTGTCTTACCTTTTGA 910
 QY 234 nGlnArgGlyAspAlaTyAlaAsnAlaAspValArgValSerLeuGlu 250
 DB 911 ACAGAGGGGTAAATAATATGCTAAAGCAATGCCAGGGTTTCATTTGGAA 959

RESULT 11

ADKS8257

ID ADKS8257 standard; DNA; 660 BP.

XX ADKS8257;

XX 06-MAY-2004 (first entry)

XX Plant DNA sequence which confers altered metabolic characteristic #5640.

XX altered metabolic characteristic; plant; acid metabolism;
 KW alcohol metabolism; fatty acid metabolism;
 KW branched fatty acid metabolism; alkaloid metabolism;
 KW amino acid metabolism; ester metabolism; glyceride metabolism;
 KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;
 KW terpene metabolism; isoprenoid metabolism; alkene metabolism;
 KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
 KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

XX Unidentified.

XX WO2003020936-A1.

XX 13-MAR-2003.

XX 30-AUG-2002; 2002WO-US027884.

XX 31-AUG-2001; 2001US-0316471P.

XX (DOWC) DOW CHEM CO.

XX (DOWC) DOW AGROSCIENCES LLC.

XX Weglarz T, Gachotte D, Blakealee B, McCreary DA, Pell RJ;

XX Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;

XX WPI; 2003-313091/30.

XX Novel genes that confer altered metabolic characteristics in Nicotiana
 PT benthamiana plants, useful for altering the levels of metabolites e.g.
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

XX Claim 1; SEQ ID NO 5640; 2576pp; English.

XX The invention comprises DNA sequences which confer an altered metabolic
 CC characteristic when they are expressed in a plant. The DNA sequences of
 CC the invention are useful for producing plants with an altered metabolic
 CC characteristic, such as: altered acid metabolism, alcohol metabolism,
 CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
 CC base metabolism, altered amino acid metabolism, altered ester metabolism,
 CC altered glyceride metabolism, altered phenolic metabolism, altered
 CC carbohydrate metabolism, altered sterol, oxygenated terpene, or
 CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
 CC metabolism, ketone or quinone metabolism. The DNA sequences of the
 CC invention may be used to provide disease resistance in a plant and gene
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a
 CC DNA sequence of the invention.

XX Sequence 660 BP; 194 A; 74 C; 168 G; 224 T; 0 U; 0 Other;

Alignment Scores:


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Db      61  GCAAGAAGAAATGCTGCTAGAGAACCCGCTCTCGACCACTCTTGCAATCAGGAATCCGGT 120
Qy      220  AspProTyAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAla 239
Db      121  GATCCTATGCAAGGCTTATGCAAACTTAGCTACCTTTTGGAGCAAGATGACTCG 180
Qy      240  TyrAlaAsnAlaAspValArgValSerLeuGluGluLeuAlaCysGlyGlnGlyHisAsp 259
Db      181  TATGCTAATGCTGATGCCAGAGTTTCACCTTGAACATATTGCAATTAATAACAGGCCATAAT 240
Qy      260  AspValSerLysLeuThrProThrAspPheAlaLeuGluSerLeuHisLysLeuGluSer 279
Db      241  GATGTCACATATCTACACCTAGTACCATCGGCATTTGAGGCATCTGCTAAAGATGGGAAGT 300
Qy      280  PheVal 281
Db      301  TTTCCT 306

RESULT 13
ADKS8255
ID      ADKS8255 standard; DNA; 329 BP.
XX
AC      ADKS8255;
XX
DT      06-MAY-2004 (first entry)
XX
DE      Plant DNA sequence which confers altered metabolic characteristic #5638.
XX
KW      altered metabolic characteristic; plant; acid metabolism;
KW      alcohol metabolism; fatty acid metabolism;
KW      branched fatty acid metabolism; alkaloid metabolism;
KW      amino acid metabolism; ester metabolism; glyceride metabolism;
KW      phenolic metabolism; carbohydrate metabolism; sterol metabolism;
KW      terpene metabolism; isoprenoid metabolism; alkene metabolism;
KW      alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
KW      quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX
OS      Unidentified.
XX
PN      WO2003020936-A1.
XX
PD      13-MAR-2003.
XX
PF      30-AUG-2002; 2002WO-US027884.
XX
PR      31-AUG-2001; 2001US-0316471P.
XX
PA      (DOWC ) DOW CHEM CO.
PA      (DOWC ) DOW AGROSCIENCES LLC.
XX
PI      Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
PI      Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX      WPI; 2003-313091/30.
XX
XX      Novel genes that confer altered metabolic characteristics in Nicotiana
XX      benthamiana plants, useful for altering the levels of metabolites e.g.
XX      acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX      Claim 1; SEQ ID NO 5638; 2576pp; English.
XX
XX      The invention comprises DNA sequences which confer an altered metabolic
XX      characteristic when they are expressed in a plant. The DNA sequences of
XX      the invention are useful for producing plants with an altered metabolic
XX      characteristic, such as: altered acid metabolism, alcohol metabolism,
XX      fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
XX      base metabolism, altered amino acid metabolism, altered ester metabolism,
XX      altered glyceride metabolism, altered phenolic metabolism, altered
XX      carbohydrate metabolism, altered sterol, oxygenated terpene, or
XX      isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
XX      metabolism, ketone or quinone metabolism. The DNA sequences of the
XX      invention may be used to provide disease resistance in a plant and gene
XX      shuffling or sexual PCR procedures. The present nucleic acid represents a

```

```

CC      DNA sequence of the invention.
XX
SQ      Sequence 329 BP; 93 A; 52 C; 88 G; 96 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.:      1-31e-26      Length:      329
Score:          368.00      Matches:      69
Percent Similarity:      82.69%      Conservative: 17
Best Local Similarity:    66.35%      Mismatches:  18
Query Match:      24.12%      Indels:      0
DB:            10          Gaps:          0

US-10-660-226-10 (1-305) x ADKS8255 (1-329)
Qy      91  LeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGly 110
Db      16  TTGAATGGACGATCTATGTACTTGTGGAATGATGGGTTCTGGAAAAACAACCTGGGA 75
Qy      111  LysIleMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGln 130
Db      76  AAGTTAATGTCCAAAGTCTCGGTTATACGTTCTTTGACTCGGACACATTTGATTGAACAG 135
Qy      131  AlaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArg 150
Db      136  GCGATGAATGGAACCTTCGTTGCAGAGATATTTGTTTCATCAGCGAGAAATTTTGTAGA 195
Qy      151  AspAsnGluSerSerValLeuArgAspLeuSerSerMetArgLeuValValAlaThr 170
Db      196  GGAAAGGAGACCGATCGCTTAAAGAGCTCTCTTCGAGGTATCAAGTTGTTGTTCCACA 255
Qy      171  GlyGlyGlyAlaValIleArgProIleAsnTrpArgTyrMetLysArgGlyLeuSerVal 190
Db      256  GGTGAGGTGCGAGTTTATAAGACCCCATTAACCTGGAAGTATATGCATATAAAGGAATCAGCATT 315
Qy      191  TrpLeuAspVal 194
Db      316  TGGCTAGATGTG 327

RESULT 14
ADR60836
ID      ADR60836 standard; cDNA; 614 BP.
XX
XX      ADR60836;
XX
DT      02-DEC-2004 (first entry)
XX
DE      Cotton cDNA sequence, SEQ ID 1617.
XX
KW      Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
KW      drought tolerance; plant disease resistance; galactomannan; lignin;
KW      plant growth regulator; heat tolerance; herbicide tolerance;
KW      homologous recombination; extreme osmotic condition tolerance;
KW      pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
KW      stress resistance.
XX
XX      Gossypium hirsutum.
XX
XX      US2004181830-A1.
XX
XX      16-SEP-2004.
XX
XX      29-JAN-2004; 2004US-00767795.
XX
XX      07-MAY-2001; 2001US-00849529.
XX      12-DEC-2001; 2001US-00021323.
XX
XX      (KOVA/) KOVALIC D K.
XX      (ZHOU/) ZHOU Y.
XX      (CAOY/) CAO Y.
XX
XX      Kovalic DK, Zhou Y, Cao Y;
XX      WPI; 2004-667718/65.
XX

```

XX New recombinant nucleic acid molecules and polypeptides from Gossypium
PT hirsutum, useful for producing plants with improved biological
PT characteristics (e.g. improved plant cold or drought tolerance).
XX
XX
XX Claim 1; SEQ ID NO 1617; 14pp; English.
XX
XX The invention relates to a recombinant polynucleotide comprising any of
CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
CC Also a recombinant polypeptide comprising any of the 58798 amino acid
CC sequences mentioned in the specification and producing a plant having an
CC improved property. Producing a plant having an improved property
CC comprises transforming a plant with a recombinant construct comprising a
CC promoter region functional in a plant cell operably joined to a
CC polynucleotide comprising a coding sequence for a polypeptide associated
CC with the property, and growing the transformed plant. The polypeptide is
CC useful for improving plant cold tolerance, manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, improving plant
CC drought tolerance, providing increased resistance to plant disease,
CC producing galactomannan (or lignin or plant growth regulators), improving
CC plant heat tolerance, improving plant tolerance to herbicides, increasing
CC the rate of homologous recombination in plants, improving plant tolerance
CC to extreme osmotic conditions or to pathogens or pests, improving yield
CC by modification of photosynthesis, modifying seed oil or protein yield
CC and/or content, improving yield by modification of carbohydrate, nitrogen
CC or phosphorus use and/or uptake, or improving yield by providing improved
CC plant growth and development under at least one stress condition. The
CC polynucleotide and polypeptide may also be used in recombinant DNA
CC constructs, in physical arrays of molecules, as plant breeding markers,
CC or in computer-based storage and analysis systems. The present sequence
CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20040181830. However only 6585
CC polynucleotide sequences were available, the remaining 52213
CC polynucleotides and all 58798 protein sequences were not present.
XX
SQ Sequence 614 BP; 170 A; 98 C; 154 G; 192 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,04e-25 Length: 614
Score: 362.50 Matches: 80
Percent Similarity: 73.72% Conservative: 21
Best Local Similarity: 58.39% Mismatches: 34
Query Match: 23.75% Indels: 2
DB: 13 Gaps: 1

US-10-660-226-10 (1-305) x ADR60836 (1-614)

QY 149 PheArgAspAsnGluSerSerValLeuArgAspLeuSerSerMetArgArgValVal 168
DB 1 TTCAGAAAGAGAGACTGAGGTATTGCAGAGGCTCTTCAAGAAACAGCTGTGTGT 60
QY 169 AlaThrGlyGlyAlaValIleArgProIleAsnTrpArgTyrMet---LysArgGly 187
DB 61 TCTACTGGCGAGGTGCAGTGTACGGATGTCACTGGGACTATATGCAGAAAGAGGG 120
QY 188 LeuSerValTrpLeuAspValProLeuAspAlaLeuAlaArgArgIleAlaLysValGly 207
DB 121 GTTGTGTCTGTTAGATTGATCCCTTTGGAAGCCTTGGCACAGAGGATTCGTCAGTAGGT 180
QY 208 ThrAlaSerArgProLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSer 227
DB 181 ACTCATCTCGTCCCTTTTGCAATATGAAACATGGCGATCCCTATCAAAAGGCTTTAAA 240
QY 228 LysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgVal 247
DB 241 CGGCTGTCTTACCTTTTGGAGCTGAGGGGTAAATAATTATGCTAAAGCAATGCCGGTT 300
QY 248 SerLeu-GluGluIleAlaCysLysGlnGlnLysAspValSerLysLeuThrProThr 267
DB 301 TCATTGTAAGAAATTTGCTGGCTTACTAGGTATTATGAGATGTATCAGATCTTACTCCAC 360

QY 267 rAspIleAlaIleGluSerLeuHisLysIleGluSerPheValIleGlu 283
DB 361 AGAGATCCCAATCGAGGCTTTGGGCACAAATGGAGTGTATCTAAAGGAG 409
RESULT 15
ID ACN52580/c
XX ACN52580 standard; cDNA; 573 BP.
XX ACN52580;
XX 02-DEC-2004 (first entry)
XX Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-N6-D8, SEQ:7361.
XX Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium;
KW variety Nucotton33B; library LIB3828; molecular tag; molecular marker;
KW genetic mapping; molecular mapping; seed germination; plant growth;
KW plant quality; plant yield; plant breeding; tissue printing; ss.
XX Gossypium hirsutum.
OS
XX US2004123340-A1.
XX 24-JUN-2004.
XX 12-DEC-2001; 2001US-00021323.
XX 14-DEC-2000; 2000US-0255619P.
XX (DEIK/) DEIKMAN J.
XX (FENG/) FENG P C C.
XX (FINC/) FINCHER K L.
XX (ZIEG/) ZIEGLER T E.
XX Deikman J, Feng PCC, Fincher KL, Ziegler TE;
XX WPI; 2004-479808/45.
XX
XX New isolated nucleic acid molecule that encodes a plant protein or its
PT fragment, useful for isolating a variety of agronomically significant
PT genes associated with plant growth, quality or yield, and as molecular
XX tags to map genes.
XX Claim 1; SEQ ID NO 7361; 34pp; English.
XX
XX The invention relates to 17880 cotton expressed sequence tags (ESTs;
CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
CC from primed or non-primed seeds from variety DP50B, mature seeds from
CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoeceum
CC tissue, developing fibres, carpel walls and septa from variety
CC Nucotton33B. The invention also relates to substantially purified
CC proteins or their fragments encoded by nucleic acid molecules of the
CC invention, and to transformed plants having a nucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC molecular tags to isolate genetic regions, to isolate genes, to map
CC genes, to determine gene function and to determine whether genes are
CC members of a particular gene family. The nucleic acid molecules may be
CC used for isolating a variety of agronomically significant genes
CC associated with plant growth, quality, yield, and could also serve as
CC links in metabolic and catabolic pathways. The nucleic acid molecules are
CC also useful for identifying genes important in initiating and maintaining
CC seed germination or that may be used to mitigate stresses encountered
CC during seed germination. The ESTs additionally enable the acquisition of
CC promoters and cis-regulatory elements which will be useful to express
CC agronomically significant genes in these tissues and/or other tissues,
CC and also permits the acquisition of molecular markers useful in breeding
CC schemes, genetic and molecular mapping, and in cloning of agronomically
CC significant genes. The nucleic acid molecules are further useful for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the presence or quantity of a protein by tissue printing. The
CC present sequence represents a specifically claimed EST isolated from a
CC cotton variety Nucotton33B androecium tissue cDNA library (LIB3828). The
CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from the US
XX patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340
SQ Sequence 573 BP; 183 A; 138 C; 86 G; 166 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.68e-24 Length: 573
Score: 347.50 Matches: 73
Percent Similarity: 75.21% Conservative: 18
Best Local Similarity: 60.33% Mismatches: 29
Query Match: 22.77% Indels: 1
DB: 13 Gaps: 1

US-10-660-226-10 (1-305) x ACNS2580 (1-573)

QY	164	ArgArgLeuValAlaThrGlyGlyGlyValAlaValIleArgProIleAsnTrpArgTyr	183
DB	568	AAACAACACTTGTCTTCTACTGTGGAGGTGCAGTTGTACTGGATGTGAACCTGGGACTAT	509
QY	184	Met---LysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAlaArgArg	202
DB	508	ATGCAGAGAAGGGGATTTGTTGGTTAGATGTACCTTTGGAGCCTTGGCACAAGG	449
QY	203	IleAlaIysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAspProTyr	222
DB	448	ATTGCTGCAGTAGGTACTCATCTCGTCCCTTTTGCATTATGAGATGGTGATCCATAT	389
QY	223	AlaMetAlaIlePheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsn	242
DB	388	ACAAAGCTTTAAACGTCTGCTTACCTTTTGGAGCAGAGGGTAAATAATTATGCTAAA	329
QY	243	AlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAspAspValSer	262
DB	328	GCAAAATGCCAGGGCTTTTCATTGTAAAGAAATTGCTGGCAAACTAGGTTATAGAGATGTATCA	269
QY	263	LysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGluSerPheValIle	282
DB	268	GATCTTACTCCAAACAGAGATCGCAATCGAGGCATTGGGACAAATTGGAGTGTATCTAAAG	209
QY	283	Glu 283	
DB	208	GAG 206	

Search completed: August 25, 2005, 20:53:50
Job time : 618 secs

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Qy	115	luValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetP	135
Db	200	AAACATTTGGGGCGTAATTTTCATTTGCGATTTGGTATATCGTTCATCAACCGGT	256
Qy	135	roSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerS	155
Db	257	CTGATATCCCATGGATTTTGAAGAAAGAGGTGAGGAAGCGCTTTGCAGATCGTGAACAC	316
Qy	155	erValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyAlaVal	175
Db	317	CGGCACATACAGAGCTGACCGCAGCTCCCTAATATATCATGCGACACAGGTGTGGGGCGG	376
Qy	175	allieArgProIleAsnTrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValP	195
Db	377	TTGACGCGACCAAAATCGAGAACTGCTTAAAAAAGGCTTGGTGATTTATTAGATGCCA	436
Qy	195	roLeuAspAlaLeuAlaArgAlaIleAlaLysValGlyThrAlaSerArgProLeuLeuA	215
Db	437	GTGTGATACACAGCTGCTCGTACCAAAAG-----GATAAAACCGCCCATCGCTAC	490
Qy	215	spGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnG	235
Db	491	AG-----GCACAAATATCCAGAGCAGTA-----CTTGAGCTTTTGTACAAA	532
Qy	235	lnArgGlyAspAlaTyrAlaAlaAlaAspValArgValSerLeuGluIleAlaCysL	255
Db	533	AGCGTCATCCGCTGTAT-----CGTGAAGTAGCA-----	561
Qy	255	ysGlnGlyHisAspAspValSerLysLeuThr-----ProThrAspIleAlaI	271
Db	562	-----GATATCATCATATTGCTGGACGAGCATATCCCAAGCAAAATGATCG	607
Qy	271	leGluSerLeuHisLysIleGluSerPheValIleGluHisThrAlaAspSerSerAlas	291
Db	608	GAGAGATTTTGAAGTGTGTGAAATATATGCTTTGGATCATGCCCAATAAATAAAAA	667
Qy	291	erAspAlaGlnAlaGlu	296
Db	668	CCGATCAACAGCTAAG	684

RESULT 2

```

US-09-596-002-11
; Sequence 11, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 14335
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte template ID No. 6632636 11
; PUBLICATION INFORMATION:
US-09-596-002-11

```

Alignment Scores:	
Pred. NO.:	4.15e-15
Score:	245.00
Length:	14335
Matches:	73
Conservative:	46
Mismatches:	76
Best Local Similarity:	32.16%
Query Match:	16.06%
DB:	4
Gap:	A

US-10-660-226-10 (1-305) x US-09-596-002-11 (1-14335)

Qy	78	LeuLeuLeuLysArg-----LysSerGluGluValLeuPheTyrLeuAsnGly-ArgC	95
Db	10794	CTTTCATTGAAGAGGTGATGTCGAAAGACAGGTAATGCCCTTATCAAAAACAAC	10853
Qy	95	s-lleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerG	115
Db	10854	CGATTTTGTGTGGACCTATGGGTGCAGGCAAAACAACGATAGCAAGCTGCTTGCCA	10913
Qy	115	luValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetP	135
Db	10914	AACATTGGGGCGGTAAATTCATTGATTCGCATTCGTATATCGTTCATCAACGGGT--	10970
Qy	135	roSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerS	155
Db	10971	CTGATATCCCATCGATTTTGAAGAAAGAGGTGAGGAAGGCTTCGAGATCGTGAAACAC	11030
Qy	155	erValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyAlaVal	175
Db	11031	CGCCACTACAAGAGCTGACCGCACTGCCTAAATTATCATGTCACAACAGTGGTGGCGCG	11090
Qy	175	allleArgProfileAsnTPrArgTyrMetLysArgGlyLeuSerValTrpIleuAspValP	195
Db	11091	TTGAGCGCCACCAAAATCGAGAACTGCTTAAAAAAGGCTTGCTGATTTATTAGATGCCA	11150
Qy	195	roLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuA	215
Db	11151	GTGTGCATACACAGCTGGCTCGTACCAAAAG-----GATAAAAACGCCCACTGCTAC	11204
Qy	215	spGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnG	235
Db	11205	AG-----GCACAAATCCACGAGCAGTA-----CTTCAGTCTTTGTGACAAA	11246
Qy	235	lnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluIleAlaCysL	255
Db	11247	AGCGTCATCGCTGTAT-----GTGAAGTAGCA-----	11275
Qy	255	ysGlnGlyHisAspAspValSerLysLeuThr-----ProThrAspIleAlaI	271
Db	11276	-----GATATCATCATATTCAGCTGGAGCAGCATATCCCAAGCAATGATCG	11321
Qy	271	leGluSerLeuHisLysIleGluSerPheValIleGluHisThrAlaAspSerSerAlaS	291
Db	11322	GAGAGATTTAGAAGTCTTGAAATATGCTTTGGATCATGCACCCCAATAAATAAAAA	11381
Qy	291	erAspAlaGlnAlaGlu	296
Db	11382	CCGATCAACACGCTAAG	11398

RESULT 3

```

US-09-328-352-2023
; Sequence 2023, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMIN
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2023
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2023

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Alignment Scores:	
Pred. No.:	1.14e-14
Score:	222.00
Percent Similarity:	65.00%
Length:	603
Matches:	51
Conservative:	27

Best Local Similarity: 42.50% Mismatches: 38
Query Match: 14.55% Indels: 4
DB: 4 Gaps: 3

US-10-660-226-10 (1-305) x US-09-328-352-2023 (1-603)

QY 96 IleTyrLeuValGlyMetMetGlySerGlySerThrValGlyLysLeuMetSerGlu 115
DB 94 ATTATTTGGTAGGGCCCATGGGGCAGGAAAAACAACCGTTGGAGCTCATTTAGCAGAA 153
QY 116 ValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetPro 135
DB 154 CTATTAGGCGCTGAATTTTAGATAGTATCATGAATATGAGCGAAGACAGGG---GCC 210
QY 136 SerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSer 155
DB 211 ACTATTCCTGGATTTTTGAAGAAAGAGGAGAGTCCGCTTCGTACGCGTGAACCTGTC 270
QY 156 ValLeuArgAspLeuSerSerMetArgLeuValValAlaThrGlyGlyAlaVal 175
DB 271 GTTTTAAATGAGCTTACTTCAAGGCAATTAGTGTGCCACAGGTGGCGGTCTATT 330
QY 176 IleArgProIleAsnTrpArgTyrMetLys---ArgGlyLeuSerValTrpLeuAspVal 194
DB 331 ACTCAGCGCTTAATCGGGAGTTTTTAAAGCAACGTGGAATCGTTTATCTATATACT 390
QY 195 ProLeuAspAlaLeuAlaArgAlaAlaLysValGlyThrAlaSerArgProLeuLeu 214
DB 391 CCTGTCGATTACACTACAAAGAACCTATCGC-----GATAAAATAGACCTTTATTA 444

RESULT 4

US-09-489-039A-3641
; Sequence 3641, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: 2709.2004001
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 1999-01-29
; SEQ ID NO 3641
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3641

Alignment Scores:
Pred. No.: 1,14e-14 Length: 603
Score: 222.00 Matches: 61
Percent Similarity: 51.05% Conservative: 36
Best Local Similarity: 32.11% Indels: 26
Query Match: 14.55% Gaps: 7
DB: 4

US-10-660-226-10 (1-305) x US-09-489-039A-3641 (1-603)

QY 94 ArgCysIleTyrLeuValGlyMetMetGlySerGlySerThrValGlyLysLeuMet 113
DB 94 CGCAATATCTTCTGGTTGGCCCTATGGGTGGCGGCAAAAGCACTATTGGGGCCAGTTA 153
QY 114 SerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGly 133
DB 154 GCCCAACAGCTCAACATGGAATTTTACGATTCATGAAGAGATTGAGAAACGCACTGGC 213
QY 134 MetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGlu 153
DB 214 ---GCTGATGGGTGGGTCTTCGATGTTGAAGGCGAAGAGCTTCCTGACCGTGAA 270
QY 154 SerSerValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGly 173

DB 271 GAGAAAAATTATCAATGAGTTGACGGAAAAACAGGGGATTGTGTCGCGACTGCGCGCGC 330
QY 174 AlaVal---IleArgProIleAsnTrpArgTyrMetLysArgGlyLeuSerValTrpLeu 192
DB 331 TCTGTAAATCCCGTGAACCGGTAAACCGTCTCTCGCGCCGCGCGGTGGTGTCTACCTG 390
QY 193 AspValProLeuAspAlaLeuAlaArgArgGlleAlaLysValGlyThrAlaSerArgPro 212
DB 391 GAAACTACGATCGAGAAGCAGTTGGCCCGTACGACGCG-----GATAAAAGCGCTCT 444
QY 213 LeuLeu-----AspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSer 230
DB 445 TTGTACAGTGCATGCGCGCTCGTGAA-----GTGCTGGAA 483
QY 231 MetLeuAlaGlnAlaArgGlyAspAlaTyrAlaAsn---AlaAspValArgValSerLeu 249
DB 484 GCGTGGCTGACGAGCGTTAACCCGCTGTATGAAGAGATCGCGATGTGACTATCCGCACA 543
QY 250 GluGluIleAlaCysLysGlnGlyHisAspAspValSerLysLeuThrProThrAspIle 269
DB 544 GACGATCAGAGTGCAGAAAGTC-----GTC 567
QY 270 AlalleGluSerLeuHisLysIleGluSer 279
DB 568 GCGAACCCAGATTATTTCATATGCTGGAAGC 597

RESULT 5

US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Alignment Scores:

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US 60/074,788
; CURRENT FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16393
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16393

Alignment Scores:
Pred. No.: 6,04e-13 Length: 555
Score: 205.50 Matches: 69
Percent Similarity: 49.29% Conservativeness: 35
Best Local Similarity: 32.70% Mismatches: 71
Query Match: 13.47% Indels: 37
DB: 4 Gaps: 8

US-10-660-226-10 (1-305) x US-09-252-991A-16393 (1-555)

QY 66 GlyHisGluAsn-----SerHisAenSerValAspGluAlaLeuLeuLys 81
Db 4 GGCCATCGCAATCGGTCGCTGATATCGAACACGTCGTCAAC----- 45
QY 82 ArgLysSerGluValLeuPheTyrLeuAenGlyArgCysIleTyrLeuValGlyMet 101
Db 46 -----CTGATCTCTCGCGCCG 63
QY 102 MetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSerPhe 121
Db 64 ATGGGTCTGGAAGAGACCACTCGCGCGCTGCTCGCAAGAGCTGTCATCTCGGTTTC 123
QY 122 PheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIlePhe 141
Db 124 AAGGACTCCGACAAAGAGATCGAACACAGCGGTGCGGC---GCCAATATCCCATGATCTTC 180
QY 142 LysValHisSerGluAlaPheArgAspAenGluSerSerValLeuArgAspLeuSer 161
Db 181 GATGTCAGGGCGAGTCCGTTTCGCGAGCGGAGCGGAGCCATGCTCACGAATCTTCG 240
QY 162 SerMetArgArgLeuValAlaThrGlyGlyAlaValIleArgProIleAenTrp 181
Db 241 GCCCGCGACGGCATGTGATCGCCACCGCGCGCGGGGTGATGCGCAGCGTAACCGC 300
QY 182 ArgTyrMetLysArg---GlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200
Db 301 CAGGTCTCGCGCGCGGTGCGCGGTGTGTACTGCTGCTGCGTCCGAGCACCAGATC 360
QY 201 ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220
Db 361 GCGCGCAGCGCGCGG-----GACCGCAACCGCCCCCTGTGTGAGAAAGCCCAACCGCGGA 414
QY 221 ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyr 240
Db 415 CAGATC-----CTCCGCGACTGATGGCGGTGCGGATCGGCTCTAC 456
QY 241 AlaAsn---AlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAsp 259
Db 457 CGCGAAATCGCGCATGTGTGTGTGAGACCGAGCAAGG---GCCCGCGCGCTGTCGTCTCCA 515
QY 260 AspValSerLysLeuThrProThrAspIleAla 270
Db 516 GGAAATTCCTCGA---ACGCCCTCGCAAGTTGCC 545

RESULT 10
US-09-252-991A-16202/c
; Sequence 16202, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16202
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16202

Alignment Scores:
Pred. No.: 6.38e-13 Length: 576
Score: 205.50 Matches: 69
Percent Similarity: 49.29% Conservativeness: 35
Best Local Similarity: 32.70% Mismatches: 71
Query Match: 13.47% Indels: 37
DB: 4 Gaps: 8

US-10-660-226-10 (1-305) x US-09-252-991A-16202 (1-576)

QY 66 GlyHisGluAsn-----SerHisAenSerValAspGluAlaLeuLeuLys 81
Db 573 GGCCATCGCAATCGGTCGCTGATATCGAACACGTCGTCAAC----- 532
QY 82 ArgLysSerGluValLeuPheTyrLeuAenGlyArgCysIleTyrLeuValGlyMet 101
Db 531 -----CTGATCTCTCGCGCCG 514
QY 102 MetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSerPhe 121
Db 513 ATGGGTCTGGAAGAGACCACTCGCGCGCTGCTCGCAAGAGCTGTCATCTCGGTTTC 454
QY 122 PheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIlePhe 141
Db 453 AAGGACTCCGACAAAGAGATCGAACACAGCGGTGCGGC---GCCAATATCCCATGATCTTC 397
QY 142 LysValHisSerGluAlaPheArgAspAenGluSerSerValLeuArgAspLeuSer 161
Db 396 GATGTCAGGGCGAGTCCGTTTCGCGAGCGGAGCGGAGCCATGCTCACGAATCTTCG 337
QY 162 SerMetArgArgLeuValAlaThrGlyGlyAlaValIleArgProIleAenTrp 181
Db 336 GCCCGCGACGGCATGTGATCGCCACCGCGCGGGGTGATGCGCAGCGTAACCGC 277
QY 182 ArgTyrMetLysArg---GlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200
Db 276 CAGGTCTCGCGCGCGGTGCGCGGTGTGTACTGCTGCTCGTCCGAGCACCAGATC 217
QY 201 ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220
Db 216 GCGCGCAGCGCGCGG-----GACCGCAACCGCCCCCTGTGTGAGAAAGCCCAACCGCGGA 163
QY 221 ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyr 240
Db 162 CAGATC-----CTCCGCGACTGATGGCGGTGCGGATCGGCTCTAC 121
QY 241 AlaAsn---AlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAsp 259
Db 120 CGCGAAATCGCGCATGTGTGTGTGAGACCGAGCAAGG---GCCCGCGCGCTGTCGTCTCCA 62
QY 260 AspValSerLysLeuThrProThrAspIleAla 270
Db 61 GGAAATTCCTCGA---ACGCCCTCGCAAGTTGCC 32

RESULT 11
US-09-107-532A-2146
; Sequence 2146, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2146:
SEQUENCE CHARACTERISTICS:
LENGTH: 537 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...537
SEQUENCE DESCRIPTION: SEQ ID NO: 2146:
US-09-107-532A-2146

Alignment Scores:
Pred. No.: 8,19e-11 Length: 537
Score: 185.50 Matches: 44
Percent Similarity: 61.34% Conservative: 29
Best Local Similarity: 36.97% Mismatches: 43
Query Match: 12.16% Indels: 3
DB: 4 Gaps: 3

US-10-660-226-10 (1-305) x US-09-107-532A-2146 (1-537)

QY 96 IleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGlu 115
DB 37 ATTTTGTGATTCGTTTCATGGCGCTGGAAACAAACAAATCGGTAAAGGGTTTAGCTCAA 96
QY 116 ValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetPro 135
DB 97 TGTTCACAAAGAGATGATGATTAGATACAAAGATTGAGGAACATATCCAAATTG--- 153
QY 136 SerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSer 155
DB 154 TCGATTGCCGAATATTTTCACTATTACGGGTGAAAAAGCTTTCGAAAAGTGGAGTCAGAT 213
QY 156 ValLeuArgPheLeuSerSerMetArgArgLeuValAlaValAlaThrGlyGlyAlaVal 175
DB 214 ATTTTAAGAAAGCTGTCAAATGAAGCAAA---ATTATCGCGACTGGTGAGGGATTGTC 270

QY 176 IleArgProIleAsnTrpArgTyrMetLys---ArgGlyLeuSerValTrpLeuAspVal 194
DB 271 CAAAGTGCAGAAATCGGCGTTTATAAAACACAGCCGATGTTCTTTACTAGAGGCA 330
QY 195 ProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeu 213
DB 331 GAAGCGGACTGCTAGTTGATCGTATCCAAACAGATGAACCGTCTATTCCGACCTTTA 387

RESULT 12

US-09-583-110-886
Sequence 886, Application US/09583110
Patent No. 6699703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/107,433
PRIORITY FILING DATE: 1998-06-30
PRIORITY APPLICATION NUMBER: US 60/085,131
PRIORITY FILING DATE: 1998-05-12
PRIORITY APPLICATION NUMBER: US 60/051,553
PRIORITY FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 886
LENGTH: 477
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-09-583-110-886

Alignment Scores:
Pred. No.: 3.45e-10 Length: 477
Score: 179.00 Matches: 62
Percent Similarity: 50.00% Conservative: 27
Best Local Similarity: 34.83% Mismatches: 63
Query Match: 11.73% Indels: 26
DB: 4 Gaps: 8

US-10-660-226-10 (1-305) x US-09-583-110-886 (1-477)

QY 98 LeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeu 117
DB 13 TTATTAGGTTTATGGGGCTGGAAATCGACTATTGCAAGA-----GCCTTG 60
QY 118 GlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerVal 137
DB 61 GACACTAATTACCTTGATATGATGCTCTGATTGAGAGCGCTAGGTATG---TCCATT 117
QY 138 AlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeu 157
DB 118 GCGAATTTTTCGCTGAAAGGGAGAGAGACCTTTGTCAGGTAGATCAGAAGTCTTA 177
QY 158 ArgAspLeuSerSerMetArgArgLeuValAlaThrGlyGlyAlaValIleArg 177
DB 178 GCTGATTACTACAAACAGACCAA---GTCGTGTCACCTGGAGGAGGTGTTATTCT 234
QY 178 ProIleAsnTrpArgTyrMetLysArgGlyLeu---SerValTrpLeuAspValProLeu 196
DB 235 CAGAGAAATCGTGACTTACTCAAGACTAATACAGATAACATCTACCTGAAGCAGATTTT 294
QY 197 AspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGln 216
DB 295 GAAACCCCTACCAACGATATCGAGCTGATAAGGCAATCAGCGACCGCTTTTCTTAAT 354
QY 217 ProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnArg 236
DB 355 AATAGCAGGAA-----GAACTAGTAGCTATTATTTTCAGAAAGA 393
QY 237 GlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGln 256


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Db 394 CAGGCTTGCTAT-----GAGGAAGTGGCTAGTCGGTT 426
QY 257 GlyHisAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeu 274
Db 427 -----TTGGATGTGTACCAAGCTAGCCAGAGAAATT---ATAGAGGAACCTA 471

RESULT 13
US-09-107-433-795
; Sequence 795, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 795:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...480
; SEQUENCE DESCRIPTION: SEQ ID NO: 795:
US-09-107-433-795

Alignment Scores:
Pred. No.: 3,48e-10 Length: 480
Score: 179.00 Matches: 62
Percent Similarity: 50.00% Conservative: 27
Best Local Similarity: 34.83% Mismatches: 63
Query Match: 11.73% Indels: 26
DB: 4 Gaps: 8

US-10-660-226-10 (1-305) x US-09-107-433-795 (1-480)
QY 98 LeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeu 117
Db 16 TTATTAGGGTTTATGGGGGCTGGAATAATCGACTATTGCAAGA-----GGCTTG 63
```

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QY 118 GlyTyrSerPheAspSerAspLysLeuValGluAlaValGlyMetProSerVal 137
Db 64 GACACTAATTCCTTATATGATGCTCTGTTGGAAGCGCCTAGGTATG---TCCATT 120
QY 138 AlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerValLeu 157
Db 121 GCGAATTTTTCGCTGAAAAGGGAGAGACCTTTTCGTAGGTAGTAATCAGAAGTCCTA 180
QY 158 ArgAspLeuSerSerMetArgGluValValAlaThrGlyGlyAlaValIleArg 177
Db 181 GCTGATTACTACAAACAGACCAA---GTCGTGTCACTGGAGGAGGATGTTATTTCT 237
QY 178 ProIleAsnTrpArgTyrMetLysArgGlyLeu---SerValTrpLeuAspValProLeu 196
Db 238 CAGAGAAATCGTGACTTACTCAAGACTAATACAGATAACATCTACTGAAACAGATTTT 297
QY 197 AspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGln 216
Db 298 GAAACCTCTACCAAGGTATCGCAGCTGATAGGACAATCAGCGACCGCTTTTCTAAAT 357
QY 217 ProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnIleArg 236
Db 358 AATAGCAAGGAA-----GAACTAGTAGCTATTATTTTCAAGAAAGA 396
QY 237 GlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluAlaCysLysGln 256
Db 397 CAGGCTTGCTAT-----GAGGAAGTGGCTAGTCGGTT 429
QY 257 GlyHisAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeu 274
Db 430 -----TTGGATGTGTACCAAGCTAAGCCAGAGAAATT---ATAGAGGAACCTA 474

RESULT 14
US-08-961-527-86/c
; Sequence 86, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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US-08-961-527-86

Alignment Scores:

Pred. No.: 1.36e-07 Length: 19390
Score: 177.00 Matches: 62
Percent Similarity: 49.44% Conservative: 26
Best Local Similarity: 34.83% Mismatches: 64
Query Match: 11.60% Indels: 26
DB: Gaps: 8

US-10-660-226-10 (1-305) x US-08-961-527-86 (1-19390)

QY 98 LeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeu 117
DB 9389 TTATTAGGTTTTCGCTGAAAGGGAGAAACAGCCTTCGTCAGTAGAATCAGAGTCTTA 9342
QY 118 GlyTyrSerPhePheAspSerAspLysLeuValGluAlaValGlyMetProSerVal 137
DB 9341 GACCCTAATTACCTTGATATGGATGCTCTGATTGAGAAATCGCTAGGTATG---TCCATT 9285
QY 138 AlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerValLeu 157
DB 9284 GCGAATTTTTCGCTGAAAGGGAGAAACAGCCTTCGTCAGTAGAATCAGAGTCTTA 9225
QY 158 ArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyAlaValIleArg 177
DB 9224 GCTGATTACTACAAACAGACCAAA---GTCGTGTCAACTGGAGGAGGTGTTATTTCT 9168
QY 178 ProIleAsnTrpArgTyrMetLysArgGlyLeu---SerValTrpLeuAspValProLeu 196
DB 9167 CAGAGAAATCGTGACTTACTCAAGACTAATACAGATAACATCTACCTGAGACGAGTTT 9108
QY 197 AspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGln 216
DB 9107 GAAACCTCTACCAAGCTATCGCAGCTGATAGGACAAATCAGCACCCTTTTCTTAAT 9048
QY 217 ProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnArg 236
DB 9047 AATAGCAAGAA---GAACTAGTAGCTATTATTTTCCAAGAAAGA 9009
QY 237 GlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGln 256
DB 9008 CAGGCTTGTTAT-----GAGAAAGTGGCTAGTCGGTT 8976
QY 257 GlyHisAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeu 274
DB 8975 -----TTGATGTGACCAAGCTAGCCAGAGGAATTT---ATAGAGGAACCTA 8931

RESULT 15

US-09-134-000C-1574
; Sequence 1574, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1574
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1574

Alignment Scores:

Pred. No.: 6.64e-09 Length: 513
Score: 167.50 Matches: 52
Percent Similarity: 48.91% Conservative: 38

Best Local Similarity: 28.26% Mismatches: 73
Query Match: 10.98% Indels: 21
DB: Gaps: 6

US-10-660-226-10 (1-305) x US-09-134-000C-1574 (1-513)

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QY 116 ValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluAlaValGlyMetPro 135
DB 76 AAATCGAAGATGCTCATCTTGAATTTAGATACAGCGTTTAATTTGAAAAAATAGAGCGC--- 132
QY 136 SerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSer 155
DB 133 TCATCTCTGACTATTTGAAAAAATATGTTGAGGAGCTTTCGAGAACAGAAACCCAA 192
QY 156 ValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyAlaVal 175
DB 193 CTTTAAAGGAGCTGTCAAAA---AATACAGCGCTCTTCACTGGGGCGGATTTGT 249
QY 176 IleArgProIleAsnTrpArgTyrMetLysArgGlyLeuSerVal---TrpLeuAspVal 194
DB 250 GTCCGACCAAGAAATCGTAGCTTATTAAATCTTTTCAGCAAGTGAATTTTATCATCGC 309
QY 195 ProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeu 214
DB 310 ACACAGAGAGCTGTTTAAAGAAATCAGAGAGATCTGAAACCAACGCGCCTTAGCT 369
QY 215 AspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGln 234
DB 370 ATAGAACGTTCTTCA-----AAAGAAATCATTACTTTGTTTGTAG 408
QY 235 GlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCys 254
DB 409 TCTCGTAAAAATTTTAT-----GAGAA-----TGT 435
QY 255 LysGlnGlyHisAspAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeu 274
DB 436 GCGAAGATGACAAATTGATCAGCAATCGTCCCGCAGAGAAATTTATCAATGAAATTCG 495
QY 275 HistyIleGlu 278
DB 496 CAACAATTAAG 507

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Job time : 762 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 25, 2005, 20:43:32 ; Search time 721 Seconds
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Delop 6.0 , Delext 7.0

Searched: 7331713 seqs, 3271544945 residues

Total number of hits satisfying chosen parameters: 14663426

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
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19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1526	100.0	1059	US-10-425-114-30672	Sequence 30672, A
2	1526	100.0	1200	US-10-660-226-9	Sequence 9, Appli
3	1457	95.5	1474	US-10-425-115-16472	Sequence 16472, A
4	1387	90.9	1228	US-10-425-114-35273	Sequence 35273, A
5	1387	90.9	1241	US-10-425-114-31574	Sequence 31574, A
6	1387	90.9	1583	US-10-425-115-16474	Sequence 16474, A
7	1351.5	88.6	1273	US-10-767-701-13420	Sequence 13420, A
8	1301.5	85.3	1410	US-10-437-963-45320	Sequence 45320, A
9	1159	76.0	1061	US-10-660-226-27	Sequence 27, Appl
10	1046	68.5	838	US-10-425-115-16473	Sequence 16473, A
11	906.5	59.4	1147	US-10-437-963-84942	Sequence 84942, A
12	881.5	57.8	1323	US-10-660-226-25	Sequence 25, Appl
13	865.5	56.7	1503	US-10-425-115-68871	Sequence 68871, A
14	860	56.4	960	US-10-660-226-19	Sequence 19, Appl
15	841	55.1	899	US-10-660-226-11	Sequence 11, Appl
16	791.5	51.9	1223	US-10-739-930-4532	Sequence 4532, Ap
17	741	48.6	738	US-10-425-115-16469	Sequence 16469, A
18	691	45.3	1256	US-10-437-963-2340	Sequence 2340, Ap
19	631.5	41.4	637	US-10-487-901-57	Sequence 57, Appl
20	625.5	41.0	1327	US-10-425-114-29872	Sequence 29872, A
21	625.5	41.0	1354	US-10-424-599-70058	Sequence 70058, A
22	620	40.6	397	US-10-437-963-84944	Sequence 84944, A
23	606.5	39.7	1332	US-10-739-930-523	Sequence 523, App
24	568	37.2	967	US-10-424-599-137299	Sequence 137299, A
25	568	37.2	967	US-10-425-114-29612	Sequence 29612, A
26	553.5	36.3	544	US-10-660-226-15	Sequence 15, Appl
27	547	35.8	536	US-10-425-114-6610	Sequence 6610, Ap
28	532.5	34.9	696	US-10-437-963-2317	Sequence 2317, Ap
29	504	33.0	1041	US-10-767-701-11266	Sequence 11266, A
30	483.5	31.7	641	US-10-739-930-1680	Sequence 1680, Ap
31	473	31.0	1010	US-10-767-795-1616	Sequence 1616, Ap
32	409	26.8	492	US-10-424-599-25738	Sequence 25738, A
33	405	26.5	657	US-10-424-599-82654	Sequence 82654, A
34	385.5	25.3	660	US-10-487-901-5640	Sequence 5640, Ap
35	376	24.6	786	US-10-424-599-70060	Sequence 70060, A
36	374	24.5	309	US-08-864-408A-8601	Sequence 8601, Ap
37	368	24.1	329	US-10-487-901-5638	Sequence 5638, Ap
38	364.5	23.9	1183	US-10-660-226-21	Sequence 21, Appl
39	362.5	23.8	614	US-10-767-795-1617	Sequence 1617, Ap
40	347.5	22.8	573	US-10-021-323-7361	Sequence 7361, Ap
41	345	22.6	1096	US-10-424-599-11365	Sequence 11365, A
42	344.5	22.6	365	US-10-425-115-151552	Sequence 151552, A
43	333	21.8	958	US-10-424-599-82116	Sequence 82116, A
44	319	20.9	1154	US-10-424-599-11361	Sequence 11361, A
45	318.5	20.9	570	US-10-369-493-26307	Sequence 26307, A

ALIGNMENTS

RESULT 1
US-10-425-114-30672
; Sequence 30672, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Kresen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28

```
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 30672
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73062D01_FLI
US-10-425-114-30672

Alignment Scores:
Pred. No.: 4,5e-167 Length: 1059
Score: 1526.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-660-226-10 (1-305) x US-10-425-114-30672 (1-1059)

QY 1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAlaAlaGlyPheGlySerSer 20
DB 29 ATGGAGCGGGGGCGCTCGCGCTGGCGCTGCAGCGCGGGCGCGGGCTTCGGCTCCAGC 88
QY 21 ArgHisArgGlyGlyLeuGlnAlaProThrGlySerLeuArgValAlaAspProAlaGly 40
DB 89 CGGACCGGGGGCGCTCAGCGGCCCCACGGGAGCTCGAGAGCTCGTACCCCGGGGGA 148
QY 41 ProAlaValAlaValArgAlaArgGlySerLysProValAlaProLeuArgLeuArgAla 60
DB 149 CTCTCGGCTGCTGTGGGGTCTCGGGGTCCAGGCCCGCTCGCACCGCTCCGACTCCGTCGG 208
QY 61 LysLysSerSerGlyGlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLeu 80
DB 209 AAGAAATCGTCCGGAGGTATGAAAACTCGCAACTCCGTTGACCAAGCTCTCTCTGTTG 268
QY 81 LysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGly 100
DB 269 AAGAGAAATCAGAGAAGTCTGTCTACTTGAACGGGAGGTGTATTTACCTAGTAGGA 328
QY 101 MetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSer 120
DB 329 ATGATCGGTTCTGGAAAAAGTACTGTGGGGAAGATTATGCTGAAGTCTTGGGTTATTCG 388
QY 121 PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140
DB 389 TTCTTTGATGATGACAAAGTTAGTGGAGCAAGCTGTGGAATGCCATCAGTTGCCCAATA 448
QY 141 PheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArgAspLeu 160
DB 449 TTCAAGTCCATAGTAGAAGCTTCTTTCGGGATAATGAGAGTAGTGTCTTTGAGAGATTG 508
QY 161 SerSerMetArgArgLeuValAlaThrGlyGlyGlyAlaValAlaValIleArgProIleAsn 180
DB 509 TCTCCTCATGCGAGATTAGTTGTTCACCGGAGGTGCTGTATTTCGACCAATAAC 568
QY 181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200
DB 569 TGGAGATATATGAAGAGGGCCCTATCTGTTGGTTAGATGTGCCCTTGGATGCTCTGTCT 628
QY 201 ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220
DB 629 AGCGGTATTGCTAAAGTGGGAATGCTCTCGTCTCTTCTGGACCAACCACTGGTGAT 688
QY 221 ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyr 240
DB 689 CCGTAGCAATGCGCTTTCTTAAGCTCAGCATGCTTGCACAGCAAAAGGGGTGATGCTTAT 748
QY 241 AlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAspAsp 260
DB 749 GCAAAATGCAGATGAAGGGTTTCTCTGGAAGAGATTGCATGTAAACAAGTCAATGAT 808
QY 261 ValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGluSerPhe 280
DB 943
```

```
DB 809 GTCTTAAGCTGACACCTACTGATATTGCAATTGAGTCACTTTATAAGATCGAGAGCTTC 868
QY 281 ValIleGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGlnSerGlnIleGln 300
DB 869 GTCATCGAGCACACTGCTGATAGTTTCAGCTAGCGACGGCAAGCTGAGTGCAGATCCAG 928
QY 301 ArgIleGlnThrLeu 305
DB 929 AGGATACAGACCTTG 943

RESULT 2
US-10-660-226-9
; Sequence 9, Application US/10660226
; Publication No. US20040064848A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Rendina, Alan
; TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
; FILE REFERENCE: BB-1159-C
; CURRENT APPLICATION NUMBER: US/10/660,226
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/09/354,501
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1200
; TYPE: DNA
; ORGANISM: Zea mays
US-10-660-226-9

Alignment Scores:
Pred. No.: 5,37e-167 Length: 1200
Score: 1526.00 Matches: 305
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-660-226-10 (1-305) x US-10-660-226-9 (1-1200)

QY 1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAlaAlaGlyPheGlySerSer 20
DB 144 ATGGAGCGGGGGCGCTCGCGCTGGCGCTGCAGCGCGGGCGGGCTTCGGCTCCAGC 203
QY 21 ArgHisArgGlyGlyLeuGlnAlaProThrGlySerLeuArgValAlaAspProAlaGly 40
DB 204 CGGACCGGGGGCGCTCAGCGGCCCCACGGGAGCTCGAGAGTGTGCTACCCCGGGGGA 263
QY 41 ProAlaValAlaValArgAlaArgGlySerLysProValAlaProLeuArgLeuArgAla 60
DB 264 CTCTCGGCTGCTGTGGGGTCTCGGGTCCAGACCGCTCGCACCGCTCCGACTCCGTCGG 323
QY 61 LysLysSerSerGlyGlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLeu 80
DB 324 AAGAAATCGTCCGGAGGTATGAAAACTCGCAACTCCGTTGACCAAGCTCTCTCTGTTG 383
QY 81 LysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGly 100
DB 384 AAGAGAAATCAGAGAAAGTCTGTCTTACTTTGAACGGGAGGTGTATTTACCTAGTAGGA 443
QY 101 MetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSer 120
DB 444 ATGATGGGTTCTGGAAAAAGTACTGTGGGAAGATTATGCTGGAAGTCTTGGGTTATTCG 503
QY 121 PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140
DB 504 TTCTTTGATGATGACAAAGTTAGTGGAGCAAGCTGTGGAATGCCATCAGTTGCCCAATA 563
```

```
QY 141 PheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArgAspLeu 160
Db 564 TTCAAGGTCCATAGTGAAGCTTCTTTCGGATAATGAGAGTAGTGTCTTGAGAGATTG 623

QY 161 SerSerMetArgGluValAlaThrGlyGlyGlyAlaValIleArgProIleAsn 180
Db 624 TCTCCATCGACGATAGTGTGTCACCGGAGGTGGTGTGTATATCCGACCAATTAAC 683

QY 181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200
Db 684 TGGAGATATATGAGAGGGCCCTATCTGTGTGTAGATGTGCCCTTGGATGCTCTTGCT 743

QY 201 ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220
Db 744 AGCGGTATTGCTAAAGTGGGAACCTGCTCTCGTCTCTTCTGGACCAACCATCTGGTGAT 803

QY 221 ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnArgGlyAspAlaTyr 240
Db 804 CCGTAGCAATGGCCCTTTCTTAAGCTCAGCATGCTTGCACAGCAAAAGGGGTGATGCTTAT 863

QY 241 AlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAspAsp 260
Db 864 GCAAAATGCAGATGTAAGGGTTTCTTGGAGAGATTGCATGTAAACAAGGTCTATGATGAT 923

QY 261 ValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGluSerPhe 280
Db 924 GTCTCTAAGCTGACACCTACTGATATTGCAATTGAGTCACTTTCATTAAGATCGAGAGCTTC 983

QY 281 ValIleGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSerGlnIleGln 300
Db 984 GTCATCGACACACTCTCATATGTTTCAGCTAGCGACGCAAGCTGAGTCGAGATCCAG 1043

QY 301 ArgIleGlnThrLeu 305
Db 1044 AGGATACAGACCTTG 1058
```

RESULT 3

```
US-10-425-115-16472
; Sequence 16472, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 16472
; LENGTH: 1474
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115020C.1
US-10-425-115-16472
```

Alignment Scores:

```
Pred. No.: 7,59e-159 Length: 1474
Score: 1457.00 Matches: 293
Percent Similarity: 96.72% Conservative: 2
Best Local Similarity: 96.07% Mismatches: 8
Query Match: 95.48% Indels: 2
DB: 20 Gaps: 1
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US-10-660-226-10 (1-305) x US-10-425-115-16472 (1-1474)

```
QY 1 MetGluAlaGlyValGlyValGluAlaLeuGlnAlaArgAlaAlaGlyPheGlySerSer 20
Db 96 ATGGAGCGGGGGCGTGGCGCTGCAGACGCGGGCGGGCGCTTCGGCTCCGGA 155
```

```
QY 21 ArgHisArgGlyGlyLeuGlnAlaProThrGlySerLeuArgValAlaAspProAlaGly 40
Db 156 CAGCGCGGGCGCGCTACAGTCCGCCATCCGGAGCCTGAGAGTCCGTGACCCGCGGA 215

QY 41 ProIleValAlaValArgAlaArgGlySerLysProValAlaProLeuArgLeuArgAla 60
Db 216 CCGTGGGTTCGGCTGCGGGTTCGCGGTCCAGACCGCTCGTACCG-----CTCCGTGG 269

QY 61 LysLysSerSerGlyGlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLeu 80
Db 270 AAGAAATCGTCCGGAGGTCAAGAACTTGCATAAATCCGTTGAGAGACATCTCTGTTG 329

QY 81 LysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGly 100
Db 330 AAGAGAAAATCAGAAAGAGTCTCTTCTTAAACCGGAGGTGATTTTACTTAGTGGGA 389

QY 101 MetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSer 120
Db 390 ATGATGGGTTCGGAAAAAGTACTGTGGGGAAGATCATGTCTGAAAGTCTTGGGTATTTCG 449

QY 121 PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140
Db 450 TTCTTTGATAGTCACAAATAGTAGGAGCAAGCTGTGGAAATGCCATCAGTTCGCCCAATA 509

QY 141 PheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArgAspLeu 160
Db 510 TTCAAGGTCCATAGTGAAGCTTCTTTCGGGATAATGAGAGTAGTGTCTTGAGAGATTG 569

QY 161 SerSerMetArgArgLeuValValAlaThrGlyGlyGlyAlaValIleArgProIleAsn 180
Db 570 TCCTCCATCGCAGCATAGTATTGTTGTCACCGGAGGTGGTGTGTTATCCGACCAATTAC 629

QY 181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200
Db 630 TGGAGATATATGAGAGGGCGCTACTGTTTGGTAGATGTGCCCTTGGATGCTCTTGCT 689

QY 201 ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220
Db 690 AGCGGTATTGCTTAAAGTGGGAACCTGCTCTCGTCTCTTTCGGACCAACCATCTGGTGAT 749

QY 221 ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyr 240
Db 750 CCGTACGCAATGGCCCTTTTCTAAGCTCAGCATGCTTGCACAGCAAGGGGTGATGCTTAT 809

QY 241 AlaAsnAlaAspValArgValSerLeuGluIleAlaCysLysGlnGlyHisAspAsp 260
Db 810 GCAAAATGCAGATGTAAAGGTTCCTCTGGAAGAGATTGCATGTAAACAAGGTCTATGATGAT 869

QY 261 ValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGluSerPhe 280
Db 870 GTCTCTAAGCTGACACCTACTGATATTGCAATTGAGTCACTTTCATAAGATCGAGAGCTTC 929

QY 281 ValIleGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSerGlnIleGln 300
Db 930 GTCATCGAGCACACTGCTGATAGTTTCAGCTAGCGACGCGCAAGCTGAGTCGAGATCCAG 989

QY 301 ArgIleGlnThrLeu 305
Db 990 AGGATACAGACCTTG 1004
```

RESULT 4

```
US-10-425-114-35273
; Sequence 35273, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 35273

; LENGTH: 1228

; TYPE: DNA

; ORGANISM: Zea mays subsp. mexicana

; FEATURE:

; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE77E09_FLI

US-10-425-114-35273

Alignment Scores:

Pred. No.: 8,09e-151 Length: 1228
Score: 1387.00 Matches: 278
Percent Similarity: 94.10% Conservative: 9
Best Local Similarity: 91.15% Mismatches: 16
Query Match: 90.89% Indels: 2
DB: 18 Gaps: 1

US-10-660-226-10 (1-305) x US-10-425-114-35273 (1-1228)

```
QY 1 MetGluAlaGlyValGlyLeuAlaLeuGlnAlaAArgAlaAlaGlyPheGlySerSer 20
Db 165 ATGAGCGGGGGCGCTGGCGCTGGCGCTGCAGACGGCGGGCGGCGCTTCGGCTCCGGC 224
QY 21 ArgHisArgGlyLeuGlnAlaProThrGlySerLeuArgValAlaAaspProAlaGly 40
Db 225 CAGCGCGGGGGCGCTACAGTCCGCCCATTTGGAGGCTGAGAGTCCGCTGAACCGGGGGA 284
QY 41 ProAlaValAlaValArgAlaAargGlySerLysProValAlaProLeuArgLeuArgAla 60
Db 285 GCTCGCGGTTCCGCTGGGGTTCCGGGCTCCAGCCGCTCGTACCG-----CTCCGTGGC 338
QY 61 LysLysSerSerGlyHisGlnAenSerHisAasnSerValAaspGluAlaLeuLeuLeu 80
Db 339 AAGAAATCATCCGGAGGTCATGAANAATTCGATAACTCCGTTGACGACGAAGCTCTCTGTTG 398
QY 81 LysArgLysSerGluValLeuPheTyrLeuAenGlnArgCysIleTyrLeuValGly 100
Db 399 AAGAGAAAATCAGAGAAGTCTCTGTCTACTTAAACGGGAGGTTATTTACTTAGTGGGA 458
QY 101 MetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSer 120
Db 459 ATGATGGGTTCTGGAAAAAGTACTGTGGGGAAGATCATGTCTGAAGTCTTGGGTTATTTCG 518
QY 121 PhePheAaspSerAaspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140
Db 519 TTCTTTGTAGTAGACAAATAGTGGAGCAAGCTGTTGGAAATGCCTTCAGTTGCTCAATA 578
QY 141 PheLysValHisSerGluAlaPhePheAaspAenGluSerSerValLeuArgAaspLeu 160
Db 579 TTCAAAGTTTCACAGTGAAGCTTCTTTTCGGATAATGAGAGTAGCGCTTTGAGGATCTG 638
QY 161 SerSerMetArgArgLeuValAlaThrGlyGlyAlaValIleArgProIleAen 180
Db 639 TCTCTCATCGACGATTAGTTGTTCACCGGAGGTGGTGTGTATCCGACCAAGTTAAC 698
QY 181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAaspValProLeuAaspAlaLeuAla 200
Db 699 TCGAAATATATGAAGAGGCCATATCCGTTTGGTTAGATGTGCCCTTGGATGCTCTGCT 758
QY 201 ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAaspGlnProSerGlyAasp 220
Db 759 AGCGGTATTGCTAAAGTGGGAAACCGCTTCTCGTCTCTTCTGGACCAACCGTCGGTGAT 818
QY 221 ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAaspAlaTyr 240
Db 819 CCATACACATGGCCCTTTCTAGCTCAGCATGCTTGCAGAGCAAGGGGTGATGCTTAT 878
QY 241 AlaAenAlaAaspValArgValSerLeuGluIleAlaCysLysGlnGlyHisAaspAasp 260
```

```
Db 879 GCAAAATCGGATGTAAAGGTTTCTCTGGAAGAGATTGCATCTAAACAAGGTCATGCGCAT 938
QY 261 ValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisIleGluSerPhe 280
Db 939 GTCTCTAAAGCTGATGCCGACTGATATCGCAATTGAGTCACCTTCATAAGATCGAGAGTTTC 998
QY 281 ValIleGluHisThrAlaAaspSerSerAlaSerAaspAlaGlnAlaGluSerGlnIleGln 300
Db 999 GTCATCGAGACCGCTGCTGATATCCAGCTAGCGAAGTCCGAAGCTGAGTCACAGATCCAA 1058
QY 301 ArgIleGlnThrLeu 305
Db 1059 AGGATACAGACCTTG 1073
```

RESULT 5

US-10-425-114-31574

; Sequence 31574, Application US/10425114

; Publication NO. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 31574

; LENGTH: 1241

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: UC-ZMFLB73191D05_FLI

US-10-425-114-31574

Alignment Scores:

Pred. No.: 8,21e-151 Length: 1241
Score: 1387.00 Matches: 278
Percent Similarity: 94.10% Conservative: 9
Best Local Similarity: 91.15% Mismatches: 16
Query Match: 90.89% Indels: 2
DB: 18 Gaps: 1

US-10-660-226-10 (1-305) x US-10-425-114-31574 (1-1241)

```
QY 1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaAArgAlaAlaGlyPheGlySerSer 20
Db 161 ATGAGGCGGGGGCGGCGCTGGCGCTGCAGACGGCGGGCGGCGCTTCGGCTCCGGC 220
QY 21 ArgHisArgGlyGlyLeuGlnAlaProThrGlySerLeuArgValAlaAaspProAlaGly 40
Db 221 CAGCGCGGGGGCGGCTACAGTCCGCCCATCCGGAGGCTGAGAGTCCGCTGAACCGGGGA 280
QY 41 ProAlaValAlaValArgAlaAargGlySerLysProValAlaProLeuArgLeuArgAla 60
Db 281 GCTCGCGGTTCCGCTGGGGTTCCGGGCTCCAGCCGCTCGTACCG-----CTCCGTGGC 334
QY 61 LysLysSerSerGlyHisGlnAenSerHisAasnSerValAaspGluAlaLeuLeuLeu 80
Db 335 AAGAAATCATCCGAGGTCATGAAAACCTTCGTTGACGAAGCTCTCTCTGTTG 394
QY 81 LysArgLysSerGluValLeuPheTyrLeuAenGlnArgCysIleTyrLeuValGly 100
Db 395 AAGAGAAAATCAGAGAAGTCTCTGTTCTACTTTAAACGGGAGGTGATTATTACTTAGTGGGA 454
QY 101 MetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSer 120
Db 455 ATGATGGGTTCTGGAAAAAGTACTGTGGGGAAGATCATGTCTGAAGTCTTGGGTTATTTCG 514
```

```
QY 121 PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140
Db 515 TTCTTTGATAGTACAAATAGTGGAGCAAGCTGTGTGGAAATGCTTTCAGTTGCTCAATA 574
QY 141 PheLysValHisSerGluAlaPhePheArgAspGlnSerSerValLeuArgAspLeu 160
Db 575 TTCAAAGTTCACAGTGAAGCTTCTTTCGGGATATAGAGTAGCGTCTTGAGGATCTG 634
QY 161 SerSerMetArgArgLeuValAlaThrGlyGlyAlaValIleArgProIleAen 180
Db 635 TCCTCCATGCACGATTAGTTGTGTCACCGAGAGTGGTGTCTATCCGACCAAGTTAAC 694
QY 181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200
Db 695 TGGAAATATATGAAGAGGCGCTTATCCGTTTGGTTAGATGTGCCCTTGGATGCTCTTGTCT 754
QY 201 ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220
Db 755 AGGCGGATTTGCTAAAGTGGNACCGCTTCTGTCCTCTTCTGGACCAAGGGTCCGGTGAT 814
QY 221 ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAtyr 240
Db 815 CCATACACAATGCGCTTTTCTAAGCTCAGCATGCTTTCGAGAGCAAGGGTGTGATGCTTAT 874
QY 241 AlaAsnAlaAspValArgValSerLeuGluIleAlaCysLysGlnGlyHisAspAsp 260
Db 875 GCAAAATGCGGATGTAAAGGTTTCTCTGGAAGAGATTGCATCTAAACAAGGTCATGCGCAT 934
QY 261 ValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisValIleGluSerPhe 280
Db 935 GTCTCTAAGCTGATGCGGACTGATATCCGANTTGAAGTCACTTCATTAAGATCGAGAGTTTC 994
QY 281 ValIleGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSerGlnIleGln 300
Db 995 GTCATCGAGCAGCTGCTGATATCCAGTACGACTAGCGACTCGCAAGCTGAGTGCACAGATCCA 1054
QY 301 ArgIleGlnThrLeu 305
Db 1055 AGGATACAGACCTTG 1069
```

RESULT 6

```
US-10-425-115-16474
; Sequence 16474, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 16474
; LENGTH: 1583
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRF4577_115022C.1
US-10-425-115-16474
```

Alignment Scores:

Pred. No.:	1,16e-150	Length:	1583
Score:	1387.00	Matches:	278
Percent Similarity:	94.10%	Conservative:	9
Best Local Similarity:	91.15%	Mismatches:	16
Query Match:	90.89%	Indels:	2
DB:	20	Gaps:	1

US-10-660-226-10 (1-305) x US-10-425-115-16474 (1-1583)

```
QY 1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAlaAlaGlyPheGlySerSer 20
Db 222 ATGGAGGCGGGGGGGCTGGCGCTCGCTGCAGACGCGGGCGCGCTTTCGGCTCCGCGC 281
QY 21 ArgHisArgGlyGlyLeuGlnAlaProThrGlySerLeuArgValAlaAspProAlaGly 40
Db 282 CAGCGCGGGGGGGCTCAGTCCGCCATCGGAGGCTGAGAGTCTGCTGAACCGGCGGA 341
QY 41 ProAlaValAlaValArgAlaArgGlySerLysProValAlaProLeuArgLeuArgAla 60
Db 342 GCTCGGTTGCGTGGGTTCCGCGGTTCCAGCCCGTCGTACCG-----CTCCGTCG 395
QY 61 LysLysSerSerGlyGlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeu 80
Db 396 AAGAAATCATCCGGAGGTCATGAAATCTGCAATCTCGTTTGAAGAAGCTCTCTCTGTTG 455
QY 81 LysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGly 100
Db 456 AAGAAATCATGAAAGAGTCTGTCTTCTTAAACGGGAGGTGATTTTACTTAGTGGGA 515
QY 101 MetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSer 120
Db 516 ATGATGGGTTCTGGAAAAAGTACTCTGGGAAGATCATGCTGGAAGTCTTGGGTTATTCG 575
QY 121 PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140
Db 576 TTCTTTGATAGTACAAATAGTGGAGCAAGCTGTGTGGAAATGCTTTCAGTTGCTCAATA 635
QY 141 PheLysValHisSerGluAlaPhePheArgAspGlnSerSerValLeuArgAspLeu 160
Db 636 TTCAAGTTTCACAGTGAAGGCTTCTTTCGGGATATAGAGTAGCGTCTTGAAGGATCTG 695
QY 161 SerSerMetArgArgLeuValAlaThrGlyGlyAlaValIleArgProIleAen 180
Db 696 TCCTCCATGCAGCAGTATAGTTGTTGCCACCGAGGTGGTGTCTATCCGACCAAGTTAAC 755
QY 181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200
Db 756 TGGAAATATATGAAGAGGCGCTATCCGTTTGGTTAGATGTGCCCTTGGATGCTCTTGTCT 815
QY 201 ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220
Db 816 AGGCGTATGTGTAAGTGGGAACCGCTTCTGTCCTCTTCTGGACCAACCGCTCCGCTGAT 875
QY 221 ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAtyr 240
Db 876 CCATACACAATGCGCTTTTCTAAGCTCAGCATGCTTTCGAGAGCAAGGGTGTGATGCTTAT 935
QY 241 AlaAsnAlaAspValArgValSerLeuGluIleAlaCysLysGlnGlyHisAspAsp 260
Db 936 GCAAAATGCGGATGTAAAGGTTTCTGGAAGAGATTGCATCTTAAACAAGGTCATGCGCAT 995
QY 261 ValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisValIleGluSerPhe 280
Db 996 GTCTCTAAGCTGATGCGGACTGATATCGCAATTTAGTCACTTCATTAAGATCGAGAGTTTC 1055
QY 281 ValIleGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSerGlnIleGln 300
Db 1056 GTCATCGAGCAGCTGCTGATATCCAGTACGAGTCCGAAAGTGTGATGCACAGATCCA 1115
QY 301 ArgIleGlnThrLeu 305
Db 1116 AGGATACAGACCTTG 1130
```

RESULT 7

```
US-10-767-701-13420
; Sequence 13420, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```


; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 13420

; LENGTH: 1273

; TYPE: DNA

; ORGANISM: Sorghum bicolor

; FEATURE:

; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS10471_1

US-10-767-701-13420

Alignment Scores:

Pred. No.: 1,14e-146 Length: 1273
Score: 1351.50 Matches: 279
Percent Similarity: 85.67% Conservative: 8
Best Local Similarity: 83.28% Mismatches: 13
Query Match: 88.56% Indels: 35
DB: 19 Gaps: 3

US-10-660-226-10 (1-305) x US-10-767-701-13420 (1-1273)

QY 1 MetGluAlaGlyValGlyLeuAlaLeuGlnAlaArg-----13
DB 122 ATGGAGCG-----GGCTGGCGCTGCAGACGCGCGCGCTTCGGCTCCGGA 172
QY 13 -----13
DB 173 CGCGCGCGGGCGCTACAGTCGCCATCGGAGCGCTGAGAGTCGCTGATCGCGGGA 232
QY 14 -----AlaAlaGlyPheGlySerSerArgHisArgGlyGlyLeuGlnAlaProThr 30
DB 233 GTCGGGTTGCCCGGGCTTCGGCTCCGACGCGCGCGGGCGGCTACAGTCGCCCATC 292
QY 31 GlySerLeuArgValAlaAspProAlaGlyProAlaValAlaValAlaArgGlySer 50
DB 293 GGGAGCGTCAGAGTCGTCATCCCGCGGAGTCGGGTTCCGTCGGGCTCGCGGTCC 352
QY 51 LysProValAlaProLeuArgLeuArgAlaLysLysSerSerGlyHisGluAsnSer 70
DB 353 AAGCCGTCGCACG-----CTCCGTGCCAAGAAATCGTCGGAGGTCATGAAACTTG 406
QY 71 HisAsnSerValAspGluAlaLeuLeuLysArgLysSerGluGluValLeuPheTyr 90
DB 407 CATTAATCCGTTGACGAAGCTCTCCGTTCGAGAGAAATCCGAGAAATCTGTCTTAC 466
QY 91 LeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGly 110
DB 467 TTGAACGGGAGGTGATTACTTAGTAGAATGATGGGTTCTGGAAAAAGTACAGTGGG 526
QY 111 LysIleMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGln 130
DB 527 AAGATTATCTCAAGTCTTGGGTATTCTGTTCTTTGACAGTCACAAATTAAGTGGACAA 586
QY 131 AlaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArg 150
DB 587 GCTGTTGGAATGCCITTCAGTTGCTCAATATTCAAGTTTCAAGTTCATAGCAAGCCTTCTTCG 646
QY 151 AspAsnGluSerSerValLeuArgAspLeuSerSerMetArgLeuValValAlaThr 170
DB 647 GATAATGACAGTAGTGTCTTGAGAGATTGTCCTCCATGCAACGATTAGTTGTGCCACC 706
QY 171 GlyGlyAlaValIleArgProIleAsnTrpArgTyrMetLysArgGlyLeuSerVal 190
DB 707 GCGCGTGGTGCTGTTATCCGACCACTTAATCGGAAATATATGAAGAAGGCCCTATCTGTT 766
QY 191 TrpLeuAspValProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSer 210
DB 767 TGGTTAGATGTCCTTGGATGCTCTTGTAGCGGTATTGCTTAAGTGGGAATCGCTCT 826
QY 211 ArgProLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSer 230

DB 827 CGTCTCTCTCTGGACCAACCATCTGGTGATCCATACACATGGCCCTTCTTAAGCTCAGC 886
QY 231 MetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGlu 250
DB 887 ATGCTTGACAGACAAAGGGGTGACCTTATGCAATATGACAGATGTAAAGGTTTCTCTAGAA 946
QY 251 GluIleAlaCysLysGlnGlyHisAspValSerLysLeuThrProThrAspIleAla 270
DB 947 GAGATTGCATCTNAGCAAGGTCACCATGATGTCCTTAAGCTGACACCCACCTGATATCGCA 1006
QY 271 IleGluSerLeuHisLysIleGluSerPheValIleGluHisThrAlaAspSerSerAla 290
DB 1007 ATTGAGTCACCTTCATAAGATCGAGAGCTTCGTGACGAGCACACTCTCTGATAATCCAGCT 1066
QY 291 SerAspAlaGlnAlaGluSerGlnIleGlnArgIleGlnThrLeu 305
DB 1067 AGCGACTCGCAAGCTGAGTCGCAGATCCAAAGGATACAGACCTTG 1111
RESULT 8
US-10-437-963-45320
; Sequence 45320, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 45320
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48297C.1
US-10-437-963-45320
Alignment Scores:
Pred. No.: 8,62e-141 Length: 1410
Score: 1301.50 Matches: 268
Percent Similarity: 90.35% Conservative: 13
Best Local Similarity: 86.17% Mismatches: 21
Query Match: 85.29% Indels: 9
DB: 19 Gaps: 4
US-10-660-226-10 (1-305) x US-10-437-963-45320 (1-1410)
QY 1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAlaAlaGlyPhe---GlySer 19
DB 76 ATGGAGGCG---GGCGTGGGCTGCGCTGAGTCGCGGGCGCGGGGTTCCGGCGGCTCC 132
QY 20 SerArgHisArgGlyGlyLeu-----GlnAlaProThrGlySerLeuArg 34
DB 133 GACCGCGCGGAGCGCGCTCTACGGCGCGAGGGCGCGCGGATCGGAGCTTGAGG 192
QY 35 ValAlaAspProAlaGlyProAlaValAlaValArgAlaArgGlySerIlyBProValAla 54
DB 193 CTCGCTGACGCGCGCGGTCGCGAAGCGCCGCTGTGTGGGTCGCGGGTCAAGCGGTCGCC 252
QY 55 ProLeuArgLeuArgAlaLysLysSerSerGlyGlyHisGluAsnSerHisAsnSerVal 74
DB 253 CCG-----CTCCGTGCCAAGAAATCGTCGGAGGTCATGAACATTGCTAATCTCGGTT 306
QY 75 AspGluAlaLeuLeuLeuLysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArg 94


```
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 16473
; LENGTH: 838
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115021C.1
US-10-425-115-16473
```

```
Alignment Scores:
Pred. No.: 2,12e-111 Length: 838
Score: 1046.00 Matches: 213
Percent Similarity: 99.07% Conservative: 0
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 68.55% Indels: 1
DB: 20 Gaps: 0
```

US-10-660-226-10 (1-305) x US-10-425-115-16473 (1-838)

```
QY 1 MetGluAlaGlyValGlyLeuAlaLeuGlnAlaArgAlaArgPheGlySerSer 20
DB 188 ATGAGCGGGGGCTCGCGCTCGCGCTCGAGCGCGGGCGCGGCTCGGCTCCAGC 247
QY 21 ArgHisArgGlyLeuGlnAlaProThrGlySerLeuArgValAlaAspProAlaGly 40
DB 248 CGGCACCGGGGGCTACAGCGGCCACCGGAGCTCGAGCTCGCTACCGCGGGGA 307
QY 41 ProAlaValAlaValArgAlaArgGlySerLysProValAlaProLeuArgLeuArgAla 60
DB 308 CCTCGCGTCTGTGCGGGCTCGCGGCTCAAGCGCGCTCGCACCGCTCCGACTCCGTCGG 367
QY 61 LysLysSerSerGlyGlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLeu 80
DB 368 AGAAATCTGCGGAGGTATGAAACTCGCAACTCTCGTGTGACAAAGCTCTCTCTGTG 427
QY 81 LysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGly 100
DB 428 AAGAGAAATCAGAAGAAGTCTGTCTACTTGAACGGGAGGTGTATTTACCTAGTAGGA 487
QY 101 MetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSer 120
DB 488 ATGATGGGTCTTGAAAAAGTACTGTGGGAAAGATTATGCTCAAGTCTTGGGTATTTCG 547
QY 121 PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140
DB 548 TCTTTTGATAGTACAAAGTTAGTGGAGCAAGCTGTTGGAATGCCATCAGTTGCCAAATA 607
QY 141 PheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArgAspLeu 160
DB 608 TTCAAGTCCATAGTGAAGCTTCTTTCGGGATAATGAGAGTAGTGTCTTGAGAGATTTC 667
QY 161 SerSerMetArgArgLeuValAlaThrGlyGlyAlaValIleArgProIleAsn 180
DB 668 TCCTCCATCGACGATTAGTTGTTCACCGGAAGTGGTGTGTATTCGACCAATTAAC 727
QY 181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200
DB 728 TGGAGATATATGAAGAGGGGCCCTATCTGTGTGGTTAGATGTGCCCTTGGATCTCTTGCT 787
QY 201 ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAsp 215
DB 788 AGSCGATTGCTAAAGT-GGAACTGCTCTCGTCTCTCTCTCTCGAC 831
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RESULT 11

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US-10-437-963-84942/c
; Sequence 84942, Application US/10437963
; Publication No. US2004012343A1
```

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 84942
; LENGTH: 1147
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_84129C.1
US-10-437-963-84942
```

```
Alignment Scores:
Pred. No.: 5,52e-95 Length: 1147
Score: 906.50 Matches: 212
Percent Similarity: 68.12% Conservative: 23
Best Local Similarity: 61.43% Mismatches: 37
Query Match: 59.40% Indels: 74
DB: 19 Gaps: 9
```

US-10-660-226-10 (1-305) x US-10-437-963-84942 (1-1147)

```
QY 1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAlaAla---GlyPheGlySer 19
DB 1147 ATGAGAGCT---AGAGCGGGGCTGCGCATGCGCGGCGGCTGTCGGGGTCGGAGCT 1091
QY 20 -SerArgHisArgGlyGlyLeuGlnAlaPro-----Th 30
DB 1090 GCGCCGGGCTGGGCGGGCGGGCGCGCGCTGTATCCGCTGGGAGAGCGCCACCGC 1031
QY 30 rGlySerLeuArgValAlaAspProAlaGlyProAlaValAlaValAlaArgAlaArgGlySe 50
DB 1030 GCGGAGCTTCGGGTCGGAGGCCCGCGACCGCGCGGCGC----- 988
QY 50 rLysProValAlaProLeuArg---LeuArgAlaLysLysSer----- 63
DB 987 -AAGCCCTCGCCCGCTGTACTGCTCAAGCGGTC-CAGAGTTTTTTTAAATGGATTGGG 930
QY 64 -----SerG1 65
DB 929 GGAAGTGTCTTCCTTCGTGTATCTGGAGTAAATGTGCACACTATATGTGTGGAAATGG 870
QY 65 Y-----GlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLysArg 82
DB 869 AGTTGTTCAGGGGCCACGACAGCTTCATTAACCTCAGTTGATGAAGCCCTCCTGTAAAGAG 810
QY 82 glySerGluGluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGlyMetMe 102
DB 809 GAAATCAGAAGAAGTTCTATTCTACTTGAACCGGCGGTGTATTATTATTTAGTTGGAATGAT 750
QY 102 rGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSerPhePh 122
DB 749 GGGCTCAGGAAGAGTACAGTTGCAAGATATATAGCCGAGGTTTTGGGTATTTCATTCT 690
QY 122 eAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIlePhePh 142
DB 689 TCACAGTGTATAAGTTGGTTGAACAAGCAGTTGGAATGCCCTTCTGTTCGCCAAATATTCAA 630
QY 142 sValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArgAspLeuSerSe 162
DB 629 GGAGCACAGTGAAGCGGTTTTTTCAGAGATAATGAGGCA----- 593
```

QY 162 rMetArgArgLeuValValAlaThrGlyGlyAlaValIleArgProIleAsnTrpAr 182
Db 592 -----ATGAA 588
QY 182 gTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAlaArgAr 202
Db 587 ATATATGAAGAAAGGCTATCTGTCTGGCTGGATGTCCTTTGGATGCACTTGCAGAGGG 528
QY 202 gIleAlaValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAspProTy 222
Db 527 TATTGCTCAAGTGGGTACTGCTCTGCTCTCTTGGATCAGCCATCGAGTATCCATA 468
QY 222 rAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAs 242
Db 467 CACAGGGGCTTCTCAAAACTCAGCATGCTTGCAGAGCAAGAGGCGGATGCTTATGAAA 408
QY 242 nAlaAspValArgValSerLeuGluIleAlaCysLysGlnGlyHisAspValSe 262
Db 407 TGCTGATGCTCGAGTTCTCTTGAAGAAATTCAGCTAAACAGGCGCATGACGATGCTC 348
QY 262 rLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGluSerPheValI1 282
Db 347 CAACTAACACCGACCGATATGCTATTGAGGCTTACTCAGATTGAGAAATTCGTAC 288
QY 282 eGluHis-----ThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSerGlnIleGlnAr 301
Db 287 CGAGCATTCACATCAAGTGGCCAGTTGGGACCTTAATAGTTGATTCGCCAGAAATCGAAG 228
QY 301 gIleGlnThrLeu 305
Db 227 GACAAAGGCGCTTG 215

RESULT 12

US-10-660-226-25

; Sequence 25, Application US/10660226

; Publication No. US20040064848A1

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca E.

; APPLICANT: Falco, S. Carl

; APPLICANT: Pamodu, Layo O.

; APPLICANT: Hitz, William D.

; APPLICANT: Rendina, Alan

; TITLE OF INVENTION: Chorismate Biosynthesis Enzymes

; FILE REFERENCE: BB-1159-C

; CURRENT APPLICATION NUMBER: US/10/660,226

; CURRENT FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US/09/354,501

; PRIOR FILING DATE: 1999-07-16

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,611

; PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 25

; LENGTH: 1323

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-10-660-226-25

Alignment Scores:

Pred. No.:	5,45e-92	Length:	1323
Score:	881.50	Matches:	183
Percent Similarity:	78.75%	Conservative:	32
Best Local Similarity:	67.03%	Mismatches:	52
Query Match:	57.77%	Indels:	6
DB:	18	Gaps:	2

US-10-660-226-10 (1-305) x US-10-660-226-25 (1-1323)

QY 14 AlaAlaGlyPheGlySerSerArgHisArgGlyGlyLeuGlnAlaProThrGlySerLeu 33
Db 22 GCCGAGGAGGATCCCCCGGCGACAGTCGCGGGGTGAGGCTGCACCAAGTCCGGC--- 78
QY 34 ArgValAlaAspProAlaGlyProAla-ValAlaValArgAlaArgGlySerLysProVa 53

Db 79 -----GCCGCGCGCTGCTCTGCGCACCGCGCGGAGCGCGAGCACCGATCCCAT 132
QY 53 1-----AlaProLeuArgLeuArgAlaLysLysSerSerGlyGlyHisGluAsnSerHi 71
Db 133 CCGTGGCGCACCCCTCAAGGCCCTGTGTGCCACAAATCGGAGGTACTTGAGAAAGCCCA 192
QY 71 sAsnSerValAspGluAlaLeuLeuLysArgLysSerGluGluValLeuPheTyrLe 91
Db 193 CTATTCTGCTGATGAGGCTCTCGTACTAAAGCAAAAGCAGAGGAGCTGCTCCCTTACCT 252
QY 91 uAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLy 111
Db 253 GAATGACCGCTGTGTTTATCTAGTTGGAATGATGGGTTCCGCAAAACTACAGTTGGAA 312
QY 111 sIleMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAl 131
Db 313 GATAATAGCTGAAGTACTAGGCTATTTCATTCTTTCAGAGTAAAGCTGGTTGAGCAGT 372
QY 131 aValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAs 151
Db 373 TGTGGCATACCGTGGTGGCTGAGATTTTTCAGGTCCACAGTGAAGCATTTCTTCAGAGA 432
QY 151 pAsnGluSerSerValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGl 171
Db 433 TAAACGAGAGTGAAGGTACTAAGGGATTTGTCTGTAATGCACCGATTAATTTGTTGCAACAG 492
QY 171 yGlyGlyAlaValIleArgProIleAsnTrpArgTyrMetLysArgGlyLeuSerValTr 191
Db 493 AGTGTGCGGTGATACGACCAATCAATGGAGTTATATGAAGAAAGGACTCATTATTTG 552
QY 191 pLeuAspValProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerAr 211
Db 553 GTTAGATGTTCCATTGGAGCGCCCTTGCAAGAGGATTCCTCGGTTGGTACTCGGTACG 612
QY 211 gProLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMe 231
Db 613 ACCCTCTGTCATCAGGAATCTGTGATCTTATGCAAGGCTATGCCAAACTTACAGC 672
QY 231 tLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGlu 251
Db 673 ACTTTTGAACAAAGATGGATTCATATGCTAATGCTATGCCGAGTTTCCCTTGAANA 732
QY 251 uIleAlaCysLysGlnGlyHisAspValSerLysLeuThrProThrAspIleAlaI1 271
Db 733 TATTGCATTCAAACAGGACATATGATGTGAATGTTACTTACCAAGTGCCTATCGCTAT 792
QY 271 eGluSerLeuHisLysIleGluSerPheValIleGlu 283
Db 793 TGAGGCATTTGCTAAAGATGGAGAGCTTTCTTACTGAG 829

RESULT 13

US-10-425-115-68871/C

; Sequence 68871, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 68871

; LENGTH: 1503

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_162804C.1

US-10-425-115-68871

```
Alignment Scores:
Pred. No.:      4,74e-90      Length:      1503
Score:          865.50      Matches:      180
Percent Similarity: 77.01%      Conservative: 31
Best Local Similarity: 65.69%      Mismatches: 39
Query Match:      56.72%      Indels:      24
DB:              20          Gaps:         2

US-10-660-226-10 (1-305) x US-10-425-115-68871 (1-1503)
QY 18 GlySerSerArgHisArgGlyLeuGlnAlaProThrGlySer-Leu----- 33
Db 1132 GCGAGGCTCGCGTTCGGCGGACAGCGCGGAGGCTGGCTGGCGCGGATAC 1073
QY 34 ----ArgValAlaAspProAlaGlyProAlaValAlaValArgAlaArgGlySerLysPr 52
Db 1072 GCGAGGCGCGGATCTCTGCC----- 1051
QY 52 oValAlaProLeuArgLeuArgAlaLysLysSerSerGlyGlyHisGluAsnSerHisAs 72
Db 1050 -----CTCGGTGGCGCGCGAATCTGCAGGAACAGAAAGGTCCACTA 1007
QY 72 nSerValAspGluAlaLeuLeuLeuLysArgLysSerGluGluValLeuPheTyrLeuAs 92
Db 1006 CTCCTGCTGATGACGCTCTCATACTACAGCAAAAGCCAGGATGTTCTGCCCTTACTTGA 947
QY 92 nGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIl 112
Db 946 TGGCCGCTTCGTTATCTGTTGGAATGATGGGTTTCAGGCAAAACTACAGTTGGGAAGAT 887
QY 112 eMetSerGluValLeuGlyTyrSerPhePheAspSerLysLeuValGluGlnAlaVa 132
Db 886 ACTATCCGAAGTGTAGGTATTCGTTCTTCACAGTGATAAGTTGGTAGAAGCGCTGT 827
QY 132 lGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAs 152
Db 826 TGGTATTTTCATCTGTTGCTGAGATCTTTCAGCTCCATAGCAAAACATCTTCAGAGATAA 767
QY 152 nGluSerSerValLeuArgAspLysSerSerMetArgArgLeuValAlaThrGlyGl 172
Db 766 TCAGAGTGAGGTCCTGAGGGATCTGTTCATCAATGCATCGCTTGGTTGGTTCACCGGAGG 707
QY 172 yGlyAlaValIleAArgProIleAsnTrpArgTyrMetLysAArgGlyLeuSerValTrpIe 192
Db 706 TGGTGAGTGATCCGACCAATCAATGGAGTTACATGAAGAAGGCTGACCGTATGGTT 647
QY 192 uAspValProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgPr 212
Db 646 AGATGTCCCATCTGGATGCACTTGCAGAGAGATCGCTGCTAGGAACCGCGTCTCGACC 587
QY 212 oLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetIe 232
Db 586 ACTCTTGATCAGGAATCTGGTGATCCTTATGCAAGGCTTATGCAAAACTTACATCACT 527
QY 232 uAlaGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluLul 252
Db 526 TTTTGGCAAGAAGATGGACTCGTATGCTAATGCTGATGCCAGATTTCATTGAACATAT 467
QY 252 eAlaCysLysGlnGlyHisAspAspValSerLysLeuThrProThrAspIleAlaIleGl 272
Db 466 TGCATTAAACAGGCGCAATATGATCTACTATCTTACCTAGTACCCTAGTACCCTGCCATTGA 407
QY 272 uSerLeuHisLysIleGluSerPheValIleGluHisThr 285
Db 406 GGCATTGCTAAAGATGGAAGTTTCTTACCGAGAAGACC 367
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RESULT 14

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US-10-660-226-19
; Sequence 19, Application US/10660226
; Publication No. US2004006484A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
```

```
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Rendina, Alan
; TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
; FILE REFERENCE: BB-1159-C
; CURRENT APPLICATION NUMBER: US/10/660,226
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/09/354,501
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Sorghum
US-10-660-226-19

Alignment Scores:
Pred. No.:      1.1e-89      Length:      960
Score:          860.00      Matches:      174
Percent Similarity: 83.40%      Conservative: 32
Best Local Similarity: 70.45%      Mismatches: 33
Query Match:      56.36%      Indels:       8
DB:              18          Gaps:         2

US-10-660-226-10 (1-305) x US-10-660-226-19 (1-960)
QY 39 AlaGlyProAlaValAlaValAlaArgGlySerLysProValAlaProLeuArgLeu 58
Db 8 GCGGCTCTGCCCTC-----CGTCCC---GCAAGCTGAGAGTT 43
QY 59 ArgAlaLysLysSerSerGlyGlyHisGluAsnSerHisAsnSerValAspGluAlaLeu 78
Db 44 TCGTCTCCGGAATCGGACGACAGCAAGAAAGTCCACTATTTCTACTGACGAGGCTCTC 103
QY 79 LeuLeuLysArgLysSerGluGluValLeuPheTyrLeuAsnGlyValArgCysIleTyrLeu 98
Db 104 ATACTACGACAAAGGCCAGGATGTTCTCCCTTACTTGGATGGCCGATGCGTTATCTT 163
QY 99 ValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGly 118
Db 164 GTTGAATGATGGGTTTCAGGCAAACTACAGTTGGAGAGATATTAGCCGAGTATTAGT 223
QY 119 TyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAla 138
Db 224 TATTGCTTCTTGACAGTGATAAGCTGGTAGAAGGCTGTTGGTATCTCATCTCTGTGT 283
QY 139 GlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArg 158
Db 284 GAGATCTTTCAGCTCCATAGTGAAGCATCTTTCAGAGATAATAGAGTAGAGTCTCTGAGG 343
QY 159 AspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyGlyValAlaValIleArgPro 178
Db 344 GATCTGTCATCAATCATCGTGGTGGTTGTGTGCAACCGGAGGTGGTGCAGTGATCCGACCA 403
QY 179 IleAsnTrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAla 198
Db 404 ATCAATTGGAGTTACATGAAGAAGGCTGACTGTGTGTTAGAGCTTTCACATGGATGCA 463
QY 199 LeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSer 218
Db 464 CTTGCAAGAAGAAATGCTGCTGTAGAACCGCATCTTCGACCACTCTTTCATCAGGAATCT 523
QY 219 GlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAsp 238
Db 524 GGTGACCTTATGCAAGGCTTATCGAAACTTATCATCATCTTTTGGAGCAAGAAGTGGAC 583
QY 239 AlaTyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHis 258
Db 584 TCGTATGCTAATGCTGATGCCAGAGTTTCACTTGAACATATTGTCATTAAACCAAGCCAT 643
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Qy 259 AspAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGlu 278
Db 644 AATGATGTCACTATCTTACACCTAGTCCTCGCCATTGAGGCAATGCTAAAGATGGA 703
Qy 279 SerPheValIleGluHisThr 285
Db 704 AGTTTCTTACCAGAGACC 724

RESULT 15

US-10-660-226-11
; Sequence 11, Application US/10660226
; Publication No. US20040064848A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hitz, William D.
; APPLICANT: Rendina, Alan
; TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
; FILE REFERENCE: BB-1159-C
; CURRENT APPLICATION NUMBER: US/10/660,226
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/09/354,501
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/093,611
; PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 899
; TYPE: DNA
; ORGANISM: Zea mays
US-10-660-226-11

Alignment Scores:
Pred. No.: 1,62e-87 Length: 899
Score: 841.00 Matches: 165
Percent Similarity: 87.50% Conservative: 31
Best Local Similarity: 73.66% Mismatches: 28
Query Match: 55.11% Indels: 0
DB: 18 Gaps: 0

US-10-660-226-10 (1-305) x US-10-660-226-11 (1-899)

Qy 62 LysSerSerGlyGlyHisGluAenSerHisAenSerValAspGluAlaLeuLeuLys 81
Db 11 CAACTGCGAGTGGAAACAGAGAGGTCCACTCTCTGCTGATGACCTCTCATCTACAG 70
Qy 82 ArgLysSerGluGluValLeuPheTyrLeuAenGlyArgCysIleTyrLeuValGlyMet 101
Db 71 CAAAAGCCAGGATGTTCTGCCTTACTTGGATGGCGGTTGCTTTATCTTGTGGATG 130
Qy 102 MetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSerPhe 121
Db 131 ATGGGTTTCAGGCAAACTACAGTTGGGAAGATATATCCGAAGTGTAGGTTATTCTGTTTC 190
Qy 122 PheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIlePhe 141
Db 191 TTCGACAGTGATAGTTGGTAGAAGGCTGTTGGTATTTCATCTGTTGCTGAGATCTTT 250
Qy 142 LysValHisSerGluAlaPhePheArgAspAenGluSerSerValneuArgAspLeuSer 161
Db 251 CAGCTCCATAGCAAAACATTCTTCAGAGATATAGAGTGAGGTCCCTGACGGATCTGTCA 310
Qy 162 SerMetArgGluValValAlaThrGlyGlyAlaValIleArgProIleAenTrp 181
Db 311 TCAATGCATCGGTGTTGTTGCAACCGGAGGTGGTGCAGTGATCCGACCAATCAATTGG 370
Qy 182 ArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAlaArg 201
Db 371 AGTTACATGAAGAGGCTGACCGGTATGGTTAGATGTCCCACTGGATGCTTGCAGA 430

Qy 202 ArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAspPro 221
Db 431 AGAATCGCTGCTGTAGGAACCGGTCTCGACCACTTTGCATCAGGAATCCGGTGATCCT 490
Qy 222 TyrAlaMetAlaPheSerLysLeuSerMetIleuAlaGlnGlnArgGlyAspAlaTyrAla 241
Db 491 TATGCAAGGCTTATGCAAACTTACGTCACCTTTTGAGCAAGAAATGGACTCGTATGCT 550
Qy 242 AsnAlaAspValArgValSerLeuGluGlnIleAlaCysLysGlnGlyHisAspAspVal 261
Db 551 AATGCTGATGCCAGAGTTTCACTTGAACATATTGCAATAAACAAGGCCATTAATGATGTC 610
Qy 262 SerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGluSerPheVal 281
Db 611 ACTATACTTACACCTAGTACCATCGCATTTGAGGCATTGCTAAAGATGGAAGTTTCTT 670
Qy 282 IleGluHisThr 285
Db 671 ACCGAGAGACC 682

Search completed: August 25, 2005, 23:32:54
Job time : 725 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 25, 2005, 20:22:28 ; Search time 3683 Seconds
(without alignments)

3152.213 Million cell updates/sec

Title: US-10-660-226-10

Perfect score: 1526

Sequence: 1 MEAGVGGLALQARAAGFGSS.....ADSSASDAQESQIQRIQTL 305

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh

-Q/cgn2_1/USPTO_spool/US10660226/runat_25082005_110427_28535/app_query.fasta_1.455

-DB=EST -Qfmt=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0

-UNITX=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US10660226 @CNC 1.1 3437 @runat_25082005_110427_28535 -NCPU=6 -ICPU=3

-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc1:*

4: gb_hc3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_g881:*

9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1346	88.2	1305	3	AY104682 Zea mays
2	1127.5	73.9	825	6	CB684025 OSJNEf113C
3	1091.5	71.5	833	6	CB657302 OSJNEc121
4	1050	68.8	667	6	CA078453 SCR1AM100
5	1043.5	68.4	809	6	CB656619 OSJNEc11D
6	1024.5	67.1	689	4	BJ248029 BJ248029
7	1013	66.4	804	7	CN147205 WOUND1_48
8	1012.5	66.3	797	6	CB641679 OSJNEB01H
9	1004	65.8	818	6	CB684026 OSJNEf113C

10	990.5	64.9	772	6	CB656558	OSJNEc11B
11	972	63.7	854	6	CB657303	OSJNEc121
12	968	63.4	640	4	BJ472228	BJ472228
13	964	63.2	672	6	CA146167	SCVPR207
14	960	62.9	609	6	AM671996	LG1_353_A
15	957	62.7	789	6	CB656559	OSJNEc11B
16	953	62.5	789	6	CB656620	OSJNEc11D
17	934	61.2	619	6	CA452817	Rp3A-3_H0
18	928.5	60.8	914	4	BG301287	HVSMB002
19	925	60.6	620	6	CF033002	QCF11b08.
20	915	60.0	814	7	CF636791	zmrww0.0
21	909	59.6	648	5	BU986135	HF09N051
22	899	58.9	650	6	CA105686	SCJFHR1C0
23	896.5	58.7	701	7	CA114633	WOUND1_23
24	891	58.4	649	1	AV909303	AV909303
25	879	57.6	733	5	CA452716	Rp3AH1_A1
26	863.5	56.6	752	5	BQ295318	WHE2868_F
27	850	55.7	582	4	BG355018	947035E10
28	848	55.6	659	6	CA112411	SCEJUB106
29	846.5	55.5	775	6	CA182703	SCEZST314
30	843	55.2	642	6	CD670151	3529_1_12
31	839	55.0	728	7	CN144547	WOUND1_23
32	836	54.8	612	6	CA118037	SCBGLR104
33	834	54.7	786	7	CR827364	zmrsub1.0
34	832	54.5	549	7	CO524949	3530_1_16
35	830	54.4	601	1	AI795555	614009G01
36	826	54.1	776	6	CA076988	SCQCAM104
37	825	54.1	559	5	BQ763798	EBR003_SQ
38	822	53.9	669	6	CA248324	SCCPL509
39	818	53.6	1066	7	CR286591	CR286591
40	812.5	53.2	645	4	BG415114	HVSMBK000
41	811	53.1	729	6	CD900974	G356_102G
42	809	53.0	811	7	CN138158	OX1_62_C0
43	805	52.8	692	4	BM736223	952058H01
44	802	52.6	513	2	AM671997	LG1_353_A
45	785	51.4	838	6	CB666891	OSJNEd16F

ALIGNMENTS

RESULT 1
AY104682

LOCUS
DEFINITION
Zea mays PCO108968 mRNA sequence.

ACCESSION
AY104682

VERSION
AY104682.1

KEYWORDS
HTC.

SOURCE
Zea mays

ORGANISM
Zea mays

REFERENCE
AUTHORS

TITLE

JOURNAL

REFERENCE
AUTHORS

TITLE

JOURNAL

COMMENT

AY104682 1305 bp mRNA linear HTC 16-OCT-2002
Zea mays PCO108968 mRNA sequence.
AY104682.1 GI:21207760
HTC.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1305)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whiteitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/buPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
2 (bases 1 to 1305)
Coe,E.H.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
Location/Qualifiers
1..1305
/organism="Zea mays"


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/mol_type="mRNA"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

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ORIGIN

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Alignment Scores:
Pred. No.: 7.38e-130 Length: 1305
Score: 1346.00 Matches: 275
Percent Similarity: 93.11% Conservativeness: 9
Best Local Similarity: 90.16% Mismatches: 19
Query Match: 88.20% Indels: 3
DB: 3 Gaps: 1

US-10-660-226-10 (1-305) x AY104682 (1-1305)

Qy 1 MetGluAlaGlyValGlyLeuAlaLeuAlaArgAlaAlaGlyPheGlySerSer 20
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Qy 21 ArgHisArgGlyLeuGlnAlaProThrGlySerLeuArgValAlaAlaAspProAlaGly 40
Db 257 CAGCGCGGGGGCGCTACAGTCCGCCATCGGAGGCTGAGAGTGCCTGAACCGGGGGA 316
Qy 41 ProAlaValAlaValArgAlaArgGlySerLysProValAlaProLeuArgLeuArgAla 60
Db 317 GCTCGCGGTTCGCGGGTTCGCGGGTTCGAGCGCGTGTACCG-----CTCCGTCGCG 370
Qy 61 LysLysSerSerGlyGlyHisGluAenSerHisAenSerValAspGluAlaLeuLeuLeu 80
Db 371 AGAAATCATCCGGAGGCTATGAAACTTGCATTAACCTGCTGAGCGAGCTCTCTGTG 430
Qy 81 LysArgLysSerGluGluValLeuPheTyrLeuAenGlyArgCysIleTyrLeuValGly 100
Db 431 AAGAGAAATCAGAGAAATGTTCTGTCTACTTAAACGGGAGGTGATTTACTTAGTGGGA 490
Qy 101 MetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSer 120
Db 491 ATGATGGTTCGTGAAAAAGTACTGTGGGAGAGATCATCTGCAAGTCTTGGGTTATTCG 550
Qy 121 PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140
Db 551 TTCTTTGATGACAAATATGAGGAGCAAGCTTTGGAAATGCCCTTCAGTTGCTCAATA 610
Qy 141 PheLysValHisSerGluAlaPhePheArgAspAenGluSerSerValLeuArgAspLeu 160
Db 611 TTCAAAGTTTCACAGTCAAGCTTCTTTTCGGGATAATGAGAGTAGCGTCTTTGAGGATCTG 670
Qy 161 SerSerMetArgArgLeuValAlaIleThrGlyGlyAlaValIleArgProIleAen 180
Db 671 TCTCCATGCGAGTATGTTGTTCACCGGAGT-TGNCCTTGTCTATCCGACCAAGTTTAC 729
Qy 181 TTPATGTYrMetLysArgGlyLeuSerValTTPLeuAspValProLeuAspAlaLeuAla 200
Db 730 TGGAAATATATGAAAGGGCCATCCGTTTGGTTAGATGTGCCCTTGGATGCTCTTGTCT 789
Qy 201 ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220
Db 790 AGCGCATTTGCTAAAGTGGGAACCGCTTCTCGTCCTCTTTCGACCAACCGTCCGGTGAT 849
Qy 221 ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnArgGlyAspAlaTyr 240
Db 850 CCATACACAAATGGCCCTTTCTAAGCTCAGCATGCTTGCAGAGCAAGGGGTGATGCTTAT 909
Qy 241 AlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAspAsp 260

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Db 910 GCARATCGGATGTAAGGGTTTCTCTGGAAGAGATGTCATTAACAAGGTCATGCGCAT 969
Qy 261 ValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGluSerPhe 280
Db 970 GTCTCTAAGCTGATGCCGACTGATATCGCAATTCAGTCACTTCAATAGATCGAGATTC 1029
Qy 281 VallieGluHisThrAlaAspSerSerAlaSerSepAlaGlnAlaGluSerGlnIleGln 300
Db 1030 GTCATCGAGCAGCTGCTGATAATCCAGCTAGCGACTCGCAAGCTGAGTACAGATCCAA 1089
Qy 301 ArgIleGlnThrLeu 305
Db 1090 AGGATACAGACCTTG 1104

RESULT 2
CB684025 825 bp mRNA linear EST 09-APR-2003
OSJNEF13C12.f OSJNEF Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEF13C12 5', mRNA sequence.
ACCESSION CB684025
VERSION CB684025.1 GI:29687750
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 825)
AUTHORS Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 2-0088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: C column: 12
Seq primer: gta aaa cga cgg cca gtc.
FEATURES
Location/Qualifiers
1..825
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEF13C12"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEF"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"

ORIGIN

Alignment Scores:
Pred. No.: 2.8e-107 Length: 825
Score: 1127.50 Matches: 234
Percent Similarity: 90.64% Conservativeness: 8
Best Local Similarity: 87.64% Mismatches: 16
Query Match: 73.89% Indels: 9
DB: 6 Gaps: 4

US-10-660-226-10 (1-305) x CB684025 (1-825)

Qy 1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAlaAlaGlyPhe---GlySer 19

```


Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

PCR Primers

FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: D column: 04
Seq primer: gta aac cga cgg cca gtc.

FEATURES

Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:39947"
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/notes="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN

Alignment Scores:
Pred. No.: 1,66e-98 Length: 809
Score: 1043.50 Matches: 217
Percent Similarity: 90.00% Conservative: 8
Best Local Similarity: 86.80% Mismatches: 16
Query Match: 68.38% Indels: 9
DB: 6 Gaps: 4

US-10-660-226-10 (1-305) x CB656619 (1-809)

QY 1 MetGluAlaGlyValGlyLeuAlaLeuGlnAlaArgAlaGlyPhe---GlySer 19
DB 68 ATGAGGCG---GGCGTGGGCTGGCGCTGCAGTCGGGGCGGGGTTTCGGCGCTCC 124
QY 20 SerArgHisArgGlyGlyLeu-----GlnAlaProThrGlySerLeuArg 34
DB 125 GACCGCGCGGAGCGGCTCTACGGCGCGGCGGGCGGGGCGGATCGGGAGCTTGAGG 184
QY 35 ValAlaAspProAlaGlyProAlaValAlaValAlaArgAlaArgGlySerLysProValAla 54
DB 185 GTGCGTGGAGCGCGCGTGGCGAGCGCGCTGTGTGGGCTCGCGGGTCCAAAGCGGTCGCC 244
QY 55 ProLeuArgLeuArgAlaLysLysSerSerGlyGlyHisGluAsnSerHisAsnSerVal 74
DB 245 CCG-----CTCGTGCCCAAGAAATCGTCGGAGGTCATGAACATTGCTAACTCGGTT 298
QY 75 AspGluAlaLeuLeuLysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArg 94
DB 299 GATGAAGCCCTCTTGTAAAGAGAAATCAGAAGAAAGTTCTCTTCTATTGTAATGGACGG 358
QY 95 CysIleTyrLeuValGlyMetMetGlySerGlySerThrValGlyLysIleMetSer 114
DB 359 TGTATTACCTAGTTGGAATGATGGGTTCTGGAAGAAAGTACTGTGGGAAAGATCATGCT 418
QY 115 GluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMet 134
DB 419 GAAGTTTGGTTATTTCGTTCTTTGATGATGAATAATGTCGAACACGCTGTGGGCATG 478
QY 135 ProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSer 154
DB 479 CCTTCAGTCGCTCAAAATTTTCAAGGTTTCATAGTGAAGCCTTCTTAGGCAATAATGAGCT 538
QY 155 SerValLeuArgAspLeuSerSerMetArgLeuValValAlaThrGlyGlyAla 174
DB 539 AGTGCTTCGAGGATTTGCTCAATCAAGCGCATTTAGTTGTTGCTACTCGAGGTGCTGCT 598
QY 175 ValIleArgProIleAsnTrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspVal 194
DB 599 GTTATCCGACGTTAACTGGAAATACATGAAGAGGGCCTATCTGTTTGGTTGATG 658

QY 195 ProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeu 214
DB 659 CCCTTGGAGCGCTCTTCTAGGCGTATTGCTAAAGTGGGACTGCTCCGCTCTTCTTA 718
QY 215 AspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGln 234
DB 719 GATCAACCATCTGGTGATCCATACAAATGGCTTTTCTAAACTCAGCATGCTCGCGGAG 778
QY 235 LysArgGlyAspAlaTyrAlaAsnAlaAsp 244
DB 779 CAAGGGCGGATGCTTTATGCAATGCTGAT 808

RESULT 6

BJ248029

LOCUS

DEFINITION

BJ248029 Y. Ogiwara unpublished cDNA library, Wh_f Triticum

acestivum cDNA clone whf4j22 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 689)

Ogiwara, Y. and Murai, K.

Expressed genes in Triticum aestivum

Unpublished (2002)

Contact: Tadabu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tsunigehis.nig.ac.jp.

Location/Qualifiers

1..689

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="whf4j22"

/tissue_type="spike at flowering date"

/dev_stage="Feekes' scale 10.5.1"

/clone_lib="Y. Ogiwara unpublished cDNA library, Wh_f"

ORIGIN

Alignment Scores:

Pred. No.: 1,29e-96 Length: 689

Score: 1024.50 Matches: 207

Percent Similarity: 93.94% Conservative: 10

Best Local Similarity: 89.61% Mismatches: 11

Query Match: 67.14% Indels: 3

DB: 4 Gaps: 2

US-10-660-226-10 (1-305) x BJ248029 (1-689)

QY 42 AlaValAlaValArgAlaArgGlySerLysProValAlaProLeuArgLeuArgAlaLys 61

DB 1 GCGGCGCGCGTGGCGGCGCGTGCAGCCGCGTGTCCCG-----CTCGCGCCCAAG 54

QY 62 LysSerSer---GlyGlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLeu 80

DB 55 AAATCGTCCGGGGAGGTCATGAGAACTTGCAATACTCCGTTGAGATGCCCTCTTGTG 114

QY 81 LysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGly 100

DB 115 AAGCAAAATCAGAAAGAGGTTCTTTCCAGTTGAATGGTCGGTGTCATCTACCTAGTTGA 174

QY 101 MetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSer 120

DB 175 ATGATGGGTTCCGGGAAAGCAGCGTCGCAAGATCTTGGCTGAAGTTTGGGTTATTCA 234

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QY 121 PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140
Db 235 TTCTTTGACAGGTGATAAAATGGTGAACAAGCTGTGGCATGCCCTTCAGTTGCTCAAAAT 294
QY 141 PheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArgAspLeu 160
Db 295 TTCAGGTTTCACAGTGAACCTTCTTCAGGGATATAGAGAGTAGTGTCTTGAGGAGATTG 354
QY 161 SerSerMetArgArgLeuValValAlaThrGlyGlyAlaValAlaIleArgProIleAsn 180
Db 355 TCTCAATCGCGGATAGTTAGTTGCTACTCGAGGTGGTGTCTTATCCGACCACTTAAC 414
QY 181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200
Db 415 TCGAAAAATATGAAAGAGACTATCTGTTTGGTGGATGTGCCCTTGGAGGCTCTTGA 474
QY 201 ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220
Db 475 AGCGTATTGCTTAAGTGGGGACTGCCTCGCTCTCTTCTAGATCAACCATCCGGCAT 534
QY 221 ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyr 240
Db 535 CCATACACAATGGCTTCTCGAAACTCAGCAGCTCGCGAGCAAAAGGGCGACGCTTAT 594
QY 241 AlaAsnAlaAspValArgValSerLeuGluIleAlaCysLysGlnGlyHisAspAsp 260
Db 595 GCAAAATGCTGATGTGAGATTTCTCTCGAAGAGATGCGCATCGAAGCTGGGCCATCGCAC 654
QY 261 ValSerLysLeuThrProThrAspIleAlaIle 271
Db 655 GTCTCTAAGCTAGCCCGATTGATATGCTCTG 687

```

RESULT 7

CN147205

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

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/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="Brix623"
/db_xref="taxon:4558"
/clones="WOUND1_48 G03_A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Wounded leaves"
/notes="Organ: Leaf; Vector: pME18S-FL3; Site_1: XhoI; Site_2: XhoI; The library was prepared from polyA+ RNA harvested from 8-day-old hydroponically grown, Brix623 sorghum seedlings. For some plants, one-half of the second leaf was crushed without damaging the midvein. For others, methyl jasmonate was added to the growth medium to a final concentration of 100 uM. Leaves were harvested 3 and 27 hr after treatment and pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGT, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

```

ORIGIN

```

Alignment Scores:
Pred. No.: 2,55e-95 Length: 804
Score: 1013.00 Matches: 201
Percent Similarity: 96.74% Conservative: 7
Best Local Similarity: 93.49% Mismatches: 7
Query Match: 66.38% Indels: 0
DB: 7 Gaps: 0

US-10-660-226-10 (1-305) x CN147205 (1-804)

QY 91 LeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGly 110
Db 3 TTGAACGGGAGGTGTATTTACTTAGTAGGAATGATGGGTCTTGGAAAAAGTACAGTGGGG 62
QY 111 LysIleMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGln 130
Db 63 AAGATTATGCTGAAGTCTTGGGTATTCGTTCTTGACAGTGACAAATTAGTGGAGCAA 122
QY 131 AlaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArg 150
Db 123 GCTGTTGGAATGCCCTTCAGTTGCTCAATAATTCAGGTTCATAGCGAAGCCTCTCTTCGG 182
QY 151 AsphenGluSerSerValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThr 170
Db 183 GATAATGAGAGTAGTGTCTTGAGAGATTGCTCCTCATGCAACGATTAGTTGTTCCACC 242
QY 171 GlyGlyGlyAlaValIleArgProIleAsnTrpArgTyrMetLysArgGlyLysSerVal 190
Db 243 GCGGTGCTGCTGTTATCCGACCAGTTAACTGGAATATATGAAGAGGCGCTATCTGT 302
QY 191 TrpLeuAspValProLeuAspAlaLeuAlaArgIleAlaLysValGlyThrAlaSer 210
Db 303 TGGTTAGGTGCCCCCTTGGATGCTCTTGAGCGTATTGCTAAAGTGGGAACGTCCTCT 362
QY 211 ArgProLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSer 230
Db 363 CGTCTCTCTCGGACCAACCATCTGGTGATCCATACACAAATGGCCCTTCTTAAGCTCAGC 422
QY 231 MetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGlu 250
Db 423 ATGCTTGAGAGCAAAAGGGTGACGCTTATGCAATGCAGATGTAAGGGTTTCTCTAGAA 482
QY 251 GluIleAlaCysLysGlnGlyHisAspAspValSerLysLeuThrProThrAspIleAla 270
Db 483 GAGATTGCACTTAAGCAAGGTCCACCATGATGTCTCTAAGCTGACACCACTGATATCGCA 542
QY 271 IleGluSerLeuHisLysIleGluSerPheValIleGluHisThrAlaAspSerSerAla 290
Db 543 ATTGAGTCACCTTCAATAGATCGAGAGCTTCGTACCGAGACACACTCTCTGATTAATCAGCT 602
QY 291 SerAspAlaGlnAlaGluSerGlnIleGlnArgIleGlnThrLeu 305

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CN147205 804 bp mRNA linear EST 01-APR-2004
WOUND1_48 G03_b1_A002 Wounded leaves Sorghum bicolor cDNA clone
WOUND1_48_G03_A002 3', mRNA sequence.

CN147205
CN147205.1 GI:45987613

Sorghum bicolor (sorghum)

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 804)

Cordonnier-Pratt M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Brady, J., Eastman, A., Miller, V., Gonzalez, M., Anfuso, C., Chhabra, D., Johnson, H., Kamran, D. and Pratt, L.H.

A Sorghum EST database: mechanically damaged and methyl

Jasmonate-treated leaves

Unpublished (2003)

Other ESTs: WOUND1_48 G03_g1_A002

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in

the Human Genome Center, University of Tokyo Institute of Medical

Science; plant material and RNA prepared at Texas A & M University;

sequencing done in the Laboratory for Genomics and Bioinformatics,

University of Georgia. Sequence ends have been trimmed to exclude

vector and regions below Phred quality 16. Three-prime sequences

are presented as their reverse complement and have been trimmed to

exclude polyA.

Seq primer: Sug3-14 (TAGTCTAGCGCGCCGCGACC)

POLYA=Yes.

Location/Qualifiers

1..804

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Db      603 AGCGACTCGCAAGCTGAGTCGCGAGATCCAAAGGATACAGACCTTG 647
RESULT 8
LOCUS   CB641679
DEFINITION OSJNEB01H04.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
ACCESSION CB641679
VERSION   1
KEYWORDS  Oryza sativa (japonica cultivar-group)
SOURCE   Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE 1 (bases 1 to 797)
AUTHORS  Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE    Large-scale identification of ESTs involved in the interaction
JOURNAL  Unpublished (2003)
COMMENT  Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 01 row: H column: 04
Seq primer: gta aaa cga cgg cca gtg.
FEATURES             source
source              1..797
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEB01H04"
/tissue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEB"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (Che
85061)"
ORIGIN
Alignment Scores:
Pred. No.:      2,84e-95      Length:      797
Score:          1012.50      Matches:    211
Percent Similarity: 90.12%      Conservative: 8
Best Local Similarity: 86.83%      Mismatches: 15
Query Match:     66.35%      Indels:     9
DB:              6          Gaps:         4
US-10-660-226-10 (1-305) x CB641679 (1-797)
Qy      1 MetGluAlaGlyValGlyLeuAlaLeuGlnAlaArgAlaGlyPhe---GlySer 19
Db      76 ATGGAGCG--GGCGTGGGCTGGCGCTGCAGTCGGCGGCGGGTTCGGCGGCTCC 132
Qy      20 SerArgHisArgGlyGlyLeu-----GlnAlaProThrGlySerLeuArg 34
Db      133 GACCGCGCGCGAGCGCGCTCTACGCGCGCGCGAGGGCGCGCGGATCGCGGAGCTTGAGG 192
Qy      35 ValAlaAspProAlaGlyProAlaValAlaValArgAlaArgGlySerLysProValAla 54
Db      193 GTGCTGAGCCGCGCGTGGGAGGCGCTGTGTGGGCTCGCGGGTCCAAAGCCGGTCCG 252
Qy      55 ProLeuArgLeuArgAlaLysLysSerSerGlyGlyHisGluAsnSerHisAsnSerVal 74

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Db      253 CCG-----CTCCGTGCCAAGAAATCGTCCGGAGGTCAATGAAACATTGCTAACTCGGTT 306
Qy      75 AspGluAlaLeuLeuLysArgLysSerGluGluValLeuPheThrLeuAsnGlyATG 94
Db      307 GATGAAGCCCTCTTCTTAAGAGAAATCAGAAAGATTTCTCTTATTTGAATGACCG 366
Qy      95 CysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSer 114
Db      367 TGTATTTTACCTAGTTGGAATGATGGTCTCTGAAAAAGTACTGTGGAAAGATCATGTCT 426
Qy      115 GluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMet 134
Db      427 GAAGTTTTGGGTATTCGTCTTTCATAGTGAATAATTGGTCGAAACAAGCTGTGGGCATG 486
Qy      135 ProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSer 154
Db      487 CTTTCAGTCGCTCAAAATTTTCAGGTTTCATAGTGAAGCTCTTTTAGGGATATGAGAGT 546
Qy      155 SerValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyAla 174
Db      547 AGTGTCCTTGAGGGAATTTGTCTCAATGAAGCGATTAGTTGTTGCTACTGGAGGTGGTCT 606
Qy      175 ValIleArgProIleAsnTyrArgTyrMetLysArgGlyLeuSerValTrpLeuAspVal 194
Db      607 GTTATCCGACCACTTAACCTGGAATACATGAAGAAGGCGCTATCTGTTGGTTGGATGG 666
Qy      195 ProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeu 214
Db      667 CCCTTGGACGCTCTTTGCTAGGCGTATTGCTAAAGTGGGACATGCTCCGCTCTTCTTA 726
Qy      215 AspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGln 234
Db      727 GATCAACCATCTGGTGATCCATACACAATGGCTTTTCTTANACTCAGCATGCTCGCGGAG 786
Qy      235 GlnArgGly 237
Db      787 CAAAGGGGC 795
RESULT 9
LOCUS   CB684026/c
DEFINITION OSJNEF13C12.r OSJNEF Oryza sativa (japonica cultivar-group) cDNA
ACCESSION CB684026
VERSION   1
KEYWORDS  Oryza sativa (japonica cultivar-group)
SOURCE   Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE 1 (bases 1 to 818)
AUTHORS  Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE    Large-scale identification of ESTs involved in the interaction
JOURNAL  Unpublished (2003)
COMMENT  Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: C column: 12
Seq primer: gga aac agc tat gac cat g.
FEATURES             source
source              1..818

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/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="OSJNEF13C12"

/tissue_type="Leaf"

/dev_stage="3 week"

/lab_host="DH10B"

/clone_lib="OSJNEF"

/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; Uninfected Control"

ORIGIN

Alignment Scores:

Pred. No.: 2,28e-94 Length: 818
Score: 1004.00 Matches: 196
Percent Similarity: 96.26% Conservative: 10
Best Local Similarity: 91.59% Mismatches: 8
Query Match: 65.79% Indels: 0
DB: 6 Gaps: 0

US-10-660-226-10 (1-305) x CB684026 (1-818)

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QY 92 AsnGlyVArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLys 111
DB 818 AATGACGGTGATTACCTAGTTGGAATGATGGTTCTGGAAGAAGTACTGTGGGAAG 759
QY 112 IleMetSerGluValLeuGlyTyrSerPhePheAppSerAspLysLeuValGluAla 131
DB 758 ATCATGCTCGAAGTTTGGGTATTCTGTTGATAGTAGTAATAATGGTCGAACAAGCT 699
QY 132 ValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAsp 151
DB 698 GTGGGATGCCCTCAGTCCTCAAAATTTCAAGGTTCAAGTGAAGCCCTTCTTTAGGGAT 639
QY 152 AsnGlySerSerValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGly 171
DB 638 AATGAGATGATGCTCTGAGGATTTGCTCAATGAAGCGATTAGTTGCTACTGGA 579
QY 172 GlyAlaValIleArgProIleAsnTrpArgTyrMetLysArgGlyLeuSerValTrp 191
DB 578 GGTGGTGCTGTTATCCGACCACTTAATCGAAATACATGAAGAAGGCGCTATCTGTTGG 519
QY 192 LeuAspValProLeuAspAlaLeuAlaArgGlyIleAlaLysValGlyThrAlaSerArg 211
DB 518 TTGATGTCCTTGGACCTCTTGTAGCGTATTGCTAAAGTGGGAGTCCCTCCCGT 459
QY 212 ProLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMet 231
DB 458 CCTCTTTTAGTCAACCATCTGGTGATCCATACAAATGGCTTTTCTTAACTCAGCATG 399
QY 232 LeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGlu 251
DB 398 CTCGGGAGCAAGGGCGCATGCTTATGCAAAATGCTGATGTGAGGGTTTCTCTTGAAGAG 339
QY 252 IleAlaCysLysGlnGlyHisPheAspValSerLysLeuThrProThrAspIleAlaIle 271
DB 338 ATTGCATCTAAACAGGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 279
QY 272 GluSerLeuHisLysIleGluSerPheValIleGluHisThrAlaAspSerSerAlaSer 291
DB 278 GAGTCGTTTCATTAAGATCCAGAACCTTTGTTCATTTGAACATACCGTTGACATCCGGTTGT 219
QY 292 AspAlaGlnAlaGluSerGlnIleGlnArgGlyLeuThrLeu 305
DB 218 GACTCCAGGCTGACTCAGGTGCTCAGAGGATACAGACCTTG 177

```

RESULT 10

CB656558

LOCUS

DEFINITION OSJNEC11B01.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA

clone OSJNEC11B01 5', mRNA sequence.

ACCESSION

CB656558

VERSION

CB656558.1 GI:29660283

KEYWORDS

EST

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 772)

Jantasuriyarat,C., Lu,G., Cowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

Large-scale identification of ESTs involved in the interaction

between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: http://genome.arizona.edu

PCR Primers

FORWARD: gta aaa cga cgg cca gtg

BACKWARD: gga aac agc tat gac cat g

Plate: 11 row: B column: 01

Seq primer: gta aaa cga cgg cca gtg.

FEATURES

source

1..772

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="OSJNEC11B01"

/tissue_type="Leaf"

/dev_stage="3 week"

/lab_host="DH10B"

/clone_lib="OSJNEC"

/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:

XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN

Alignment Scores:

Pred. No.: 5,44e-93 Length: 772
Score: 990.50 Matches: 207
Percent Similarity: 89.92% Conservative: 7
Best Local Similarity: 86.97% Mismatches: 15
Query Match: 64.91% Indels: 9
DB: 6 Gaps: 4

US-10-660-226-10 (1-305) x CB656558 (1-772)

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QY 1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAlaAlaGlyPhe---GlySer 19
DB 68 ATGAGGGCG---GGCGTGGGGCTGGCGTCCAGTCGCGGGCGGGGTTCCGGCGCTCC 124
QY 20 SerArgHisArgGlyGlyLeu-----GlnAlaProThrGlySerLeuArg 34
DB 125 GACCCGCCCGGAGCGCGCTCTACCGCGCGGAGGGCGCGCGGATCGGGAGCTTGAGG 184
QY 35 ValAlaAspProAlaGlyProAlaValAlaValAlaArgAlaArgGlySerLysProValAla 54
DB 185 GTCCGTGAGCGCGCGTGGCGAAGCCCGCTGTGTGGGCTCCGGGTCGAAGCCGGTCGCC 244
QY 55 ProLeuArgLeuArgAlaLysSerSerGlyGlyHisGluAsnSerHisAsnSerVal 74
DB 245 CCG-----CTCCGTGCCAAGAAATCGTCGGAGGTCTATGAACATTGCTAACTCGGTT 298
QY 75 RepGluAlaLeuLeuLysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArg 94
DB 299 GATGAAGCCCTCTTCTAAGAGAGAAATCAGAAAGAGTTCTTCTTATTGATTGACCG 358
QY 95 CysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSer 114

```

Db 359 TGATTACCTAGTCTGGAATGATGGTTCTGGAAGAAAGTACTGTGGAAAGATCATGTCT 418
 QY 115 GluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMet 134
 Db 419 GAAGTTTGGTTATTTCGTTCTTTGATGATGAATAATTTGGTGAACAAGCTGTGGCARG 478
 QY 135 ProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheAspPheAspGluSer 154
 Db 479 CCTTCAGTCGCTCAAAATTTTCAAGGTTTCATAGTGAAGCCTTCTTTAGGGAATATGAGACT 538
 QY 155 SerValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyAla 174
 Db 539 AGTGTCCTGAGGAGATTGTCCTCAATGAAGCGATTAGTTGTGCTACTCGAGGTGGTGTCT 598
 QY 175 ValIleArgProIleAsnTyrMetLysArgGlyLeuSerValTyrLeuAspVal 194
 Db 599 GTTATCCGACCATTAACCTGGAATATACATGAAGAGGGCTATCTGTTGGTGGATGG 658
 QY 195 ProLeuAspAlaLeuAlaArgIleAlaLysValGlyThrAlaSerArgProLeuLeu 214
 Db 659 CCTTGGAGCGCTCTTGCTAGGCGTATTGCTAAAGTGGGACTGCCTCCCGTCTCTTCTA 718
 QY 215 AspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeu 232
 Db 719 GATCAACCATCTGGTGATCCATACACTATGGCTTTTCTTAAACTCATCATGCTC 772

RESULT 11
 CB657303/c
 LOCUS
 DEFINITION OSUNEC12117.1 OSUNEC Oryza sativa (japonica cultivar-group) cDNA
 clone OSUNEC12117 3', mRNA sequence.
 CB657303
 CB657303.1 GI:29661028

OSUNEC12117.1 OSUNEC Oryza sativa (japonica cultivar-group) cDNA
 clone OSUNEC12117 3', mRNA sequence.
 CB657303
 CB657303.1 GI:29661028
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoideae; Oryza.
 1 (bases 1 to 854)
 Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
 Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
 Large-scale identification of ESTs involved in the interaction
 between rice and Magnaporthe grisea
 Unpublished (2003)
 Contact: Rod Wing
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu

PCR Primers
 FORWARD: gta aaa cga cgg cca gtc
 BACKWARD: gga aac agc tat gac cat g
 Plate: 12 row: I column: 17
 Seq primer: gga aac agc tat gac cat g.
 Location/Qualifiers
 1. .854
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="OSUNEC12117"
 /tissue_type="Leaf"
 /dev_stage="3 week"
 /lab_host="DH10B"
 /clone_lib="OSUNEC"
 /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
 XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

FEATURES

source

Alignment Scores:

Pred. No.: 5,38e-91 Length: 854
 Score: 972.00 Matches: 191
 Percent Similarity: 95.71% Conservative: 10
 Best Local Similarity: 90.95% Mismatches: 0
 Query Match: 63.70% Indels: 0
 DB: 6 Gaps: 0

US-10-660-226-10 (1-305) x CB657303 (1-854)

QY 96 ILeTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGlu 115
 Db 853 ATTTACCTAGTTGGAATGATGGTTCTGAAAGAAAGTACTGTGGAAAGATCATGTCTGAA 794
 QY 116 ValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetPro 135
 Db 793 GTTTTGGGTTATTCTGTTCTTTGATGATGATAAATTTGGTGAACAAGCTGTGGGCATGCTT 734
 QY 136 SerValAlaGlnIlePheLysValHisSerGluAlaPhePheAspAspAsnGluSerSer 155
 Db 733 TCAGTCGCTCAAAATTTTCAAGGTTTCATAGTGAAGCCTTCTTTAGGATATAATGAGAGTACT 674
 QY 156 ValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyAlaVal 175
 Db 673 GTCTTGAAGGATTTGCTCTCAATGAAGCGATTAGTTGTGCTACTGGAGGTGGTGTCTGTT 614
 QY 176 ILeArgProIleAsnTyrArgTyrMetLysArgGlyLeuSerValTyrLeuAspValPro 195
 Db 613 ATCCGACCATTTACTGGAATATCATGAAGAGGGCCCTATCTGTTGGTGGATGTGCC 554
 QY 196 LeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAsp 215
 Db 553 TTGGAGCGCTCTTGCTAGGCGTATTGCTAAAGTGGGACTGCCTCCGCTCTCTTTAGAT 494
 QY 216 GlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGln 235
 Db 493 CAACCATCTGGTGATCCATACACAATGGCTTTTAACTCAGCATGCTCGCGAGCAA 434
 QY 236 ArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluLuleAlaCysLys 255
 Db 433 AGGGCGGATGCTTATGCAATGCTGATGTAGGGTTTCTTTGAAGAGNTGTCATCTAAA 374
 QY 256 GlnGlyHisAspAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHis 275
 Db 373 CAGGCTCATGATGATGATCGAAGCTAACACCACTGACATGCTATTGAGTGGTTTCAT 314
 QY 276 LysIleGluSerPheValIleGluHisThrAlaAspSerSerAlaSerAspAlaGlnAla 295
 Db 313 AAGATCGAAGACTTTGTCATTGAACATACCGTTGCAATCCGGTTGGTGGTACTCCAGGCT 254
 QY 296 GluSerGlnIleGlnArgIleGlnThrLeu 305
 Db 253 GACTCACGCTGCAGAGGATACAGACCTTG 224

RESULT 12

BJ472228

LOCUS

DEFINITION

heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA

clone baal32015 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Hordeum.

1 (bases 1 to 640)

Sato,K., Saisho,D. and Takeda,K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

CONTACT: Tadao Shin-i

BJ472228 640 bp mRNA linear EST 23-MAY-2002
 BJ472228 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,
 heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
 clone baal32015 5', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

ORGANISM
 Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.

1 (bases 1 to 640)

Sato,K., Saisho,D. and Takeda,K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadao Shin-i

ORIGIN

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

source

1. .640
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Haruna Nijo"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baal32015"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"

ORIGIN

Alignment Scores:

Pred. No.: 9,49e-91 Length: 640
Score: 968.00 Matches: 191
Percent Similarity: 96.63% Conservative: 10
Best Local Similarity: 91.83% Mismatches: 7
Query Match: 63.43% Indels: 0
DB: 4 Gaps: 0

US-10-660-226-10 (1-305) x BJ472228 (1-640)

QY 76 GluAlaLeuLeuLeuLysArgLysSerGluValLeuPheThrLeuAsnGlyArgCys 95
Db 3 GATGCCCTCTTGTGAAGAGAAATCAGAAGAGTCTTTTCAGTTGAAACGGCGGTGC 62
QY 96 IleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGlu 115
Db 63 ATCTACCTAGTTGGAATGATGGTTCGGGMAAAGCACGGTGGGAAGATCTTGGCTGAA 122
QY 116 ValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetPro 135
Db 123 GTTTTGGGTATTCTGTTTACAGTGATAATTGGTCGAACAAAGCTCTTGGCATGCT 182
QY 136 SerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSer 155
Db 183 TCAGTTGCTCAATTTTCAAGGTTACAGTGAAGCTTCTTCAGGGATATGAGAGTAGT 242
QY 156 ValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyAlaVal 175
Db 243 GTCTTGAGGATTTGTCTCTATCGCGCATTAGTTGTTGCTACTGGAGGTGGTGTGT 302
QY 176 IleArgProIleAsnTrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValPro 195
Db 303 ATCCGACCAAGTTAACTGSAATAATATGAAGAAGCGCTATCTGTTTGGTTGGATGTGCC 362
QY 196 LeuAspAlaLeuAlaArgGileAlaLysValGlyThrAlaSerArgProLeuLeuAsp 215
Db 363 TTGAAGACTCTTGCAAGGGATTGTGAAGTGGGACTGCTCGGCTCTCTTCTAGAT 422
QY 216 GlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGln 235
Db 423 CAACCATCCGGCGATCCATACACAAATGGCTTTTCGAAACTCAGCACCCCTCGCGGAGCA 482
QY 236 ArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLys 255
Db 483 AGGGGGATGCTTATGCAAAATGCTGATGTACAGATTCTCTTGAAGAGATTGCATCTAAG 542
QY 256 GlnGlyHisAspAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHis 275
Db 543 CTGGGTTCATGACGATGCTCTTAAGCTGACACCAATTGATATGCTCTTGTAGTCCGTCCAC 602
QY 276 LysIleGluSerPheValIleGlu 283
Db 603 AAGATCGAGAGCTTTTGTCTGTCGAA 626

RESULT 13

CA146167

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

COMMENT

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-660-226-10 (1-305) x CA146167 (1-672)

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

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QY

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QY

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QY

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QY

Db

QY

Db

QY

Db

QY

Db

CA146167
SCVPRT2077E07.g RT2 Saccharum officinarum cDNA clone SCVPRT2077E07
5', mRNA sequence.
CA146167
CA146167.1 GI:35044937
EST.
Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.

1 (bases 1 to 672)
Vettore,A.L., da Silva,P.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: paruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 077 row: E Column: 07
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .672
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCVPRT2077E07"
/lab_host="DH10B"
/clone_lib="RT2"
/note="Organ: Root tips (0.3cm-long) from adult plants;
Vector: pSport1; Site 1: SalI; Site 2: NotI; An
unidirectional cDNA library generated from [root
tips (0.3cm-long) from adult plants]. cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucset.lad.ic.unicamp.br/public"

Alignment Scores:
Pred. No.: 2.66e-90 Length: 672
Score: 964.00 Matches: 193
Percent Similarity: 95.24% Conservative: 7
Best Local Similarity: 91.90% Mismatches: 8
Query Match: 63.11% Indels: 2
DB: 6 Gaps: 1

US-10-660-226-10 (1-305) x CA146167 (1-672)

QY 1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAlaAlaGlyPheGlySerSer 20
Db 47 ATGAGAGCGGGGGGGCGTGGCGCTGCAGACGCGGGCGGGGCTTCGGCTCCACC 106

QY 21 ArgHisArgGlyGlyLeuGlnAlaProThrGlySerLeuArgValAlaAspProAlaGly 40
Db 107 CGGCGCGGGGGGGCGCTACAGTCCCGCAGCGCAGCTGAGAGTCTGGCCCGTCGGA 166

QY 41 ProAlaValAlaValArgAlaArgGlySerLysProValAlaProLeuArgLeuArgAla 60
Db 167 GCAGCGGTTGTGTGCGGGCTCGCGGTCGAAGCCCGTCGCACCG-----CTCCGTGG 220

QY 61 LysLysSerSerGlyGlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLeu 80
 |||||
 Db 221 AAGAAATCGTTCGGTGGTCATGAAACTTCGCATAACTCCGTTGACGAAGCTCTCCTATTG 280

QY 81 LysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGly 100
 |||||
 Db 281 AAGAGAAATCAGAAAGTCTTGTCTACTCTGAACGGGAGGTATTTACTTAGTAGGA 340

QY 101 MetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSer 120
 |||||
 Db 341 ATGATGGTCTCGAAAAAGTACCGTGGGAAGATTATGCTGAAGCTCTTGGGTATTG 400

QY 121 PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140
 |||||
 Db 401 TTCTTCGATAGTCACAAATTAGTGAGCAAGCTGTTGGAATGCTTCAGTTGCCCAATA 460

QY 141 PheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArgAspLeu 160
 |||||
 Db 461 TTCAAGGTTTCATAGCGAAGCTCTTTTCGGGATAATGAGAGTAGTGTCTTGAGAGATNG 520

QY 161 SerSerMetArgArgLeuValAlaThrGlyGlyValAlaValIleArgProIleAsn 180
 |||||
 Db 521 TCCTTCATCGGACGATTAGTGTTCGCCACCGAGGTGGTGTCTTATCCGACGATTAC 580

QY 181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200
 |||||
 Db 581 TGGCAATATATGAAGAAGGACTATCTGTTGGTTAGATGTGCCCTTGGATGCTCTNGCT 640

QY 201 ArgArgIleAlaLysValGlyThrAlaSer 210
 |||||
 Db 641 AAGCGTATTGCTAAAGTGGGAAGTGCCTCT 670

RESULT 14
 AW671996
 LOCUS LG1_353_A11.b1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
 DEFINITION
 ACCESSION AW671996
 VERSION AW671996.1 GI:7535901
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 609)
 Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H.
 An EST database from Sorghum: light-grown seedlings
 Contact: Cordonnier-Pratt MM
 Unpublished (2000)
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmp@atuga.edu
 Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 15. The threshold for highest quality sequence is 20.

Seq primer: JEN REV
 High quality sequence stop: 607
 POLYA=No.

FEATURES

Location/Qualifiers

1..609
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /db_xref="taxon:4558"
 /clone_lib="Light Grown 1 (LG1)"
 /notes="Organ: 10- to 14-day-old light-grown (greenhouse) seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were

prepared by mass excision."

ORIGIN
 Alignment Scores:
 Pred. No.: 6 09e-90 Length: 609
 Score: 960.00 Matches: 191
 Percent Similarity: 97.51% Conservatives: 5
 Best Local Similarity: 95.02% Mismatches: 3
 Query Match: 62.91% Indels: 2
 DB: 2 Gaps: 1
 US-10-660-226-10 (1-305) x AW671996 (1-609)

QY 42 AlaValAlaValArgAlaArgGlySerLysProValAlaProLeuArgLeuAlaLys 61
 |||||
 Db 12 GCGGTTGCGTGGCGGCTCGCGGCTCAAGCCCGTCGACCG-----CTCCGTCGAAG 65

QY 62 LysSerSerGlyGlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLys 81
 |||||
 Db 66 AAATCGTTCCGAGGCTCATGAAAACTTCGATAACTCCGTTGACGAAGCTCTCCTGTTGAAG 125

QY 82 ArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGlyMet 101
 |||||
 Db 126 AGAAATCCGAAGAAGTCTGTTCTACTTGAACGGGAGGTATTTACTTAGTAGGAATG 185

QY 102 MetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSerPhe 121
 |||||
 Db 186 ATGGGTTCTGGAAAAAGTACAGTGGGAAGATTATGTCCTGAAGTCTTGGGTTATTGTTTC 245

QY 122 PheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIlePhe 141
 |||||
 Db 246 TTTGACAGTCACAAATTAGTGAGCAAGCTGTGTGAATGCCCTTCAGTTGCTCAATATTTC 305

QY 142 LysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArgAspLeuSer 161
 |||||
 Db 306 AAGGTTTCATAGCAAGCTCTTTTCGGGATATAGAGTAGTGTCTTGAAGATTTGTCTC 365

QY 162 SerMetArgArgLeuValAlaThrGlyGlyGlyAlaValIleArgProIleAsnTrp 181
 |||||
 Db 366 TCCATGCAACGATTAGTTGTTGCCACCGCGGTGCTGTGTATCCGACGACGTTAACTGG 425

QY 182 ArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAlaArg 201
 |||||
 Db 426 AATAATATGAAGAAGGCTATCTCTTGGTTAGATGTGCCCTTCGATGCTCTTCGCTAGG 485

QY 202 ArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAspPro 221
 |||||
 Db 486 CGTATTGCTAAAGTGGGAAGTCCCTCTCGTCTCTCTCTGGACCAACCATCTCGTGATCCA 545

QY 222 TyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyrAla 241
 |||||
 Db 546 TACACAATGGCCTTCTTAAGCTCAGCATGCTTGCAGAGCAAGGGGTGACGCTTATGCA 605

QY 242 Aen 242
 |||||
 Db 605 AAT 608

RESULT 15

CB656559/c

LOCUS

CB656559

DEFINITION

clone OSJNEC11B01 3', mRNA sequence.

ACCESSION

CB656559

VERSION

CB656559.1

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaeae; Oryza.

1 (bases 1 to 789)

REFERENCE

1 Jantacuriyarac,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

CB656559 789 bp mRNA linear EST 09-APR-2003
 OSJNEC11B01.r OSJNEC Oryza sativa (japonica cultivar-group) cDNA
 clone OSJNEC11B01 3', mRNA sequence.

CB656559.1 GI:29660284

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaeae; Oryza.

1 (bases 1 to 789)

Jantacuriyarac,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

TITLE	Large-scale identification of ESTs involved in the interaction between rice and <i>Magnaporthe grisea</i>
JOURNAL	Unpublished (2003)
COMMENT	Contact: Rod Wing

FEATURES
SOURCE

ORIGIN

Alignment Scores:	
Pred. No.:	1,798-89
Score:	957.00
Percent Similarity:	95.65%
Best Local Similarity:	90.82%
Query Match:	62.71%
DB:	6
Length:	789
Matches:	188
Conservative:	10
Mismatches:	9
Indels:	0
Gaps:	0

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2005, 10:33:33 ; Search time 64 Seconds
(without alignments)
2440.377 Million cell updates/sec

Title: US-10-660-226-10
Perfect score: 1526
Sequence: 1 MEAGGVGLALQARAAGFGSS.....ADSSASDAQESQIRIQTL 305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_prot.*

2: uniprot_tmbl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	852	55.8	287	Q7X7H9	Oryza sativa
2	655	42.9	303	Q8GT76	Arabidopsis
3	649.5	42.6	292	AROK ARATH	Arabidopsis
4	642.5	42.1	300	AROK LYCES	Arabidopsis
5	606.5	39.7	300	Q8GV88	Arabidopsis
6	440	28.8	157	Q6PLR3	Cucumis sat
7	429	28.1	305	Q9SVA4	Arabidopsis
8	340.5	22.3	190	Q7VE85	Prochloroc
9	338.5	22.2	177	Q7NH27	Gloeobacter
10	338.5	22.2	181	Q8YXG9	Anabaena sp
11	331.5	21.7	280	Q9LW20	Arabidopsis
12	318.5	20.9	189	AROK STNY3	Synechocyst
13	312.5	20.5	191	Q7U469	Synechococ
14	311.5	20.4	183	AROK SYNEL	Synechococ
15	283	18.5	192	Q7V904	Prochloroc
16	272.5	17.9	185	Q7V3G8	Prochloroc
17	267.5	17.5	244	Q89XW7	Bradyrhizob
18	262	17.2	175	Q7ABL5	Geobacter s
19	256.5	16.8	203	Q6NCG8	Rhodospirillum rubrum
20	254.5	16.7	210	Q6GIN9	Bartonella
21	250	16.4	210	Q6GLH5	Bartonella
22	249.5	16.3	168	AROK AQUAE	Aquifex ae
23	246	16.1	265	Q655K8	Oryza sativa
24	242.5	15.9	174	Q67N09	Symbiodactyl
25	239.5	15.7	171	Q8RAE8	Thermotoga
26	237.5	15.6	492	ARXK THEM	Thermotoga
27	235	15.4	180	Q6FT84	Acinetobact
28	235	15.4	211	Q82TC0	Nitrosomon
29	234.5	15.4	200	Q9A435	Caulobacter
30	228.5	15.0	184	Q7NZU3	Chromobacte
31	227	14.9	186	Q7MUD6	Porphyromon

32	226	14.8	291	2	Q7F2E6	Oryza sativa
33	225.5	14.8	185	2	Q7VRN2	Candidatus
34	224.5	14.7	192	2	Q92ME6	Rhizobium m
35	224	14.7	173	1	AROK YERPE	Oryza sativa
36	224	14.7	173	1	Q664L9	Oryza sativa
37	223.5	14.6	174	1	AROK VIBCH	Oryza sativa
38	222	14.5	173	2	Q6CZQ8	Oryza sativa
39	220	14.4	200	2	Q8FY59	Oryza sativa
40	219.5	14.4	171	1	AROK SHEON	Oryza sativa
41	217	14.2	170	1	AROK NEIMA	Oryza sativa
42	217	14.2	170	1	AROK NEIMB	Oryza sativa
43	217	14.2	172	1	AROK SALTU	Oryza sativa
44	217	14.2	172	1	AROK SALTU	Oryza sativa
45	217	14.2	173	1	AROK PHOLL	Oryza sativa

ALIGNMENTS

RESULT 1

ID	Q7X7H9	PRELIMINARY;	PRT;	287 AA.
AC	Q7X7H9: Q7XPG2;			
DT	01-OCT-2003 (Tremblrel. 25, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	OSJNB0079B02.2 protein (OSJNB0003B01.21 protein)			
GN	Name=OSJNB0079B02.2; Synonyms=OSJNB0003B01.21;			
OS	Oryza sativa (japonica cultivar-group)			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzaceae; Oryza.			
OX	NCBI TaxID=39947;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	Pubmed12447439; DOI=10.1038/nature01183;			
RA	Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,			
RA	Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Yang K., Yu S., Tang Y.,			
RA	Weng Q., Zhang L., Lu Y., Mu J., Zhang L.S., Yu Z., Fan D.,			
RA	Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,			
RA	Wu M., Zhang B., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,			
RA	Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang X.,			
RA	Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,			
RA	Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,			
RA	Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,			
RA	Han B.;			
RT	"Sequence and analysis of rice chromosome 4."			
RL	Nature 420:316-320(2002).			
DR	EMBL; AL606455; CAE02970.2; -			
DR	EMBL; AL606649; CAE03630.2; -			
DR	HSSP; P24167; 1KAG.			
DR	Gramene; Q7X7H9; -			
DR	Gramene; Q7XPG2; -			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004765; P:shikimate kinase activity; IEA.			
DR	GO; GO:0008652; P:amino acid biosynthesis; IEA.			
DR	InterPro; IPR000623; Shik kinase.			
DR	PRINTS; PR01100; SHIKIMINASE.			
DR	PROSITE; PS01128; SHIKIMATE KINASE; 1.			
SQ	SEQUENCE 287 AA; 31211 MW; 3F2BFA8A03F661CE CRC64;			

Query Match 55.8%; Score 852; DB 2; Length 287;
Best Local Similarity 64.1%; Pred. No. 2.4e-57;
Matches 182; Conservative 37; Mismatches 61; Indels 4; Gaps 4;

QY	1	MEAGGVGLALQARA-AGFGSSNRHGGLOAQTGSLRVADPAGPAVAVRAGSKPVLRLR 59
Db	1	MDA-GVGLRAKPGAWAGLNPRRSSTARPV-FFAVERKFAQPLVLGSDRRSCG-AKLKVS 57
QY	60	AKKSGGSHNSHNSVDEALLKKKSEEVLFYNGRCIVLVGMGSGKSTVGKIMSEVLGY 119
Db	58	CSRKPAKIDKTYTYSADAELVLKQKAEDVVPYLVNDRICIVLVGMGSGKTTVGKILAEVLGY 117


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ID AROK_LYCES STANDARD; PRT; 300 AA.
AC Q00497;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Shikimate kinase, chloroplast precursor (EC 2.7.1.71).
OS Lycopersicon esculentum (tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. UC82B; TISSUE=Leaf;
RX MEDLINE=93272054; PubMed=1338949;
RA Schmid J., Schaller A., Leibinger U., Boll W., Amrhein N.;
RT "The in-vitro synthesized tomato shikimate kinase precursor is
RT enzymatically active and is imported and processed to the mature
RT enzyme by chloroplasts."
RL Plant J. 2:375-383(1992).
CC -!- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC fifth step.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- SIMILARITY: Belongs to the shikimate kinase family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X63560; CAA45121.1; -.
DR PIR; S21584; S21584.
DR HSP; P10880; ISHK.
DR InterPro; IPR000623; Shik_kinase.
DR Pfam; PF01202; SKI; 1.
DR PRINTS; PR01100; SHIKIMTKINASE.
DR PROSITE; PS01128; SHIKIMATE_KINASE; 1.
KW Aromatic amino acid biosynthesis; ATP-binding; Chloroplast; Kinase;
FT TRANSFERASE; transit peptide.
FT CHAIN 67 300 Chloroplast (Potential).
FT NP BIND 111 118 ATP (By similarity).
SQ SEQUENCE 300 AA; 33720 MW; 9CDAC8136922CCE3 CRC64;

Query Match 42.1%; Score 642.5; DB 1; Length 300;
Best Local Similarity 60.3%; Pred. No. 3.2e-41;
Matches 126; Conservative 35; Mismatches 47; Indels 1; Gaps 1;

QY 73 SVDEALLAKRKEEVLYLNGRCIVLVGMGSKSTVGKIMSEVLGYSPFSDSKLVEQAV 132
DB 84 SIDEIETLNKRAEEVEYLDGRCVYLVMGCGCKTGVGRILAEITLGYSPFDCDLIEQAV 143

QY 133 GMPVSAQIFKVAIEAFRRNNESSVLRLDSSMRLLVATGGAVIRPINRMYKRGSLVWL 192
DB 144 GGITVAIEIFELRGESFRDNETVELHKLSLMHLVLVSTGGAVRIPINRHHMKIGSVWL 203

QY 193 DVPDLALARRIAKVGTASRLDQPSGDPYANAFSKLSMLAQORGDAYANADVRSLEEI 252
DB 204 DVPLEALAKRITTEGKSRPLLHEESGDVYDTTLKRLTTLMETRGENYANASARVLENI 263

QY 253 ACKQGHDDVSKLPTPTDIAIESLHKIESFV 281
DB 264 ALKR-EKDVCHITPAETILEVLQIENFL 291

RESULT 5
Q8GY88 PRELIMINARY; PRT; 300 AA.
ID Q8GY88
AC Q8GY88;

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DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Putative shikimate kinase (Atg39540).
GN Name=Atg39540/F23K16_170;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ihida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Heuan Y.W.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK117791; BAC42436.1; -.
DR EMBL; BT005291; AAO63355.1; -.
DR HSP; P10880; ISHK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004765; F:shikimate kinase activity; IEA.
DR GO; GO:0008652; P:amino acid biosynthesis; IEA.
DR InterPro; IPR000623; Shik_kinase.
DR InterPro; IPR001680; WD40-
DR PRINTS; PR01100; SHIKIMTKINASE.
DR PROSITE; PS01128; SHIKIMATE_KINASE; UNKNOWN_1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Kinase.
SQ SEQUENCE 300 AA; 33777 MW; 8868B7DF6FF7D492 CRC64;

Query Match 39.7%; Score 606.5; DB 2; Length 300;
Best Local Similarity 55.6%; Pred. No. 1.9e-38;
Matches 130; Conservative 37; Mismatches 58; Indels 9; Gaps 5;

QY 57 RLRA---KKSSGCHENS---HNSVD-EALLAKRKEEVLYLNGRCIVLVGMGSKSTV 109
DB 55 RLRSVSDKNSSALLTGTSLHSPFDEEQILKKAAEVKPYLNGRSMYLVGMGSKTIV 114

QY 110 GKIMSEVLGYSPFSDSKLVEQAVGMPVSAQIFKVAIEAFRRNNESSVLRLDSSM-RLVW 168
DB 115 GKIMARSLGYTTFDCDTLIEQAMKGTVAEIFEHFGESVFEKEATEALKKLSIMYHQVV 174

QY 169 ATGGAGVIRPINRMYKRGSLVWLVDLALARRIAKVGTASRPLL-DOPSGDPYANAFS 227
DB 175 STGGAGVIRPINRMYKRGSLVWLVDLALARRIAKVGTASRPLL-DOPSGDPYANAFS 234

QY 228 KLSMLAQORGDAYANADVRSLEIEACKQGHDDVSKLPTPTDIAIESLHKIESFV 281
DB 235 RLSTTWDARGEATYKASARVLENTLKLGYRSVSDLPFAETAEAFEQVQSVL 288

RESULT 6
Q6PLR3 PRELIMINARY; PRT; 157 AA.
ID Q6PLR3
AC Q6PLR3
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Shikimate kinase (Fragment).
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.

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OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim M.S., Yang K.Y., Kim Y.C., Cho B.H.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY596190; AAT02351.1; -.
DR HSSP; P24167; 1KAG.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004765; F:shikimate kinase activity; IEA.
DR GO; GO:0008652; P:amino acid biosynthesis; IEA.
DR InterPro; IPR000623; Shik_kinase.
DR Pfam; PF01202; SKI; 1.
DR PRINTS; PR01100; SHIKIMTKINASE.
DR PROSITE; PS01128; SHIKIMATE_KINASE; 1.
KW Kinase.
FT NON TER
SQ SEQUENCE 157 AA; 17514 MW; 378B1863D8F9E7F2 CRC64;

Query Match 28.8%; Score 440; DB 2; Length 157;
Best Local Similarity 58.2%; Pred. No. 5.4e-26;
Matches 85; Conservative 27; Mismatches 34; Indels 0; Gaps 0;

QY 136 SVAQIFKHSEAFPRDNESVLRDLSSMRRLVVATGGGAVIRPINRWYMKRGLSVWLDVP 195
Db 3 SVAEVEKVVGEDFFREREATELRKLSLMRQFVISTGGGAVTRSNWYMHKGISVWLDVP 62

QY 196 LDALARIKVGTSAPRLDQPSGDPYAMAFSKLSMLAQOQGDYANADRVVSLEIACK 255
Db 63 LEALVVRISAVGTNSRPLHDSNDAYSKTIVRLSTLLEERGEAYANAEVKVSCAKIAK 122

QY 256 QGHDDVSKLTPDTIAIESLHKIESFV 281
Db 123 LGTKDVSNVTPMAIAIELEEIEITFL 148

RESULT 7
Q95VA4 PRELIMINARY; PRT; 305 AA.
AC Q95VA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Shikimate kinase-like protein.
GN Name=ATG39540;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL078620; CAB44689.1; -.
DR EMBL; AL161595; CAB80617.1; -.
DR PIR; T09370; T09370.
DR HSSP; P10880; 1SHK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004765; F:shikimate kinase activity; IEA.
DR GO; GO:0008652; P:amino acid biosynthesis; IEA.
DR InterPro; IPR000623; Shik_kinase.
DR InterPro; IPR001680; WD40.
DR PRINTS; PR01100; SHIKIMTKINASE.
DR PROSITE; PS01128; SHIKIMATE_KINASE; UNKNOWN_1.
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DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Kinase.
SQ SEQUENCE 305 AA; 34744 MW; 9C08637565F59FC CRC64;

Query Match 28.1%; Score 429; DB 2; Length 305;
Best Local Similarity 53.3%; Pred. No. 8.5e-25;
Matches 88; Conservative 28; Mismatches 47; Indels 2; Gaps 2;

QY 119 YSFFSDSKLVEQAVCMPSVAQIFKHSEAFPRDNESVLRDLSSMRRLVVATGGGAVIR 177
Db 129 YGKIACDTLIEQAMKGTSAEIFEHFGESVFREKETEALKKLSLMYHQVWVSTGGGAVIR 188

QY 178 PINRWYMKRGLSVWLDVPLDALARIKVGTSAPRLDQPSGDPYAMAFSKLSMLAQO 236
Db 189 PINWYMHKGISVWLDVPLDALARIKVGTSAPRLDQPSGDPYAMAFSKLSMLAQO 248

QY 237 GDYANADRVVSLEIACKQGHDDVSKLTPDTIAIESLHKIESFV 281
Db 249 GEAYTKASARVSNLENTLKLGYRSVSDUTPAEIAIEAFEQVQSYL 293

RESULT 8
Q7VE85 PRELIMINARY; PRT; 190 AA.
AC Q7VE85;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Shikimate kinase.
GN Name=arOK; OrderedLocNames=Pro0128;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SARG / CCMP 1375 / SS120;
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufresne A., Salanoubat M., Partensky F., Attiguenave F., Amann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Wolf Y.I., Hess W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal oxphototrophic genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025 (2003).
DR EMBL; AF017161; AAP99174.1; -.
DR HSSP; P24167; 1KAG.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004765; F:shikimate kinase activity; IEA.
DR GO; GO:0008652; P:amino acid biosynthesis; IEA.
DR InterPro; IPR000623; Shik_kinase.
DR PROSITE; PS01128; SHIKIMATE_KINASE; 1.
KW Complete proteome; Kinase.
SQ SEQUENCE 190 AA; 21555 MW; 827831CEB8C141AF CRC64;

Query Match 22.3%; Score 340.5; DB 2; Length 190;
Best Local Similarity 39.8%; Pred. No. 3e-18;
Matches 80; Conservative 34; Mismatches 68; Indels 19; Gaps 4;

QY 81 KRKSEVLFLYNGRCIYLVGMWGSGKSTVTKIMSVLGYSPFSDSKLVEQAVCMPSVAQI 140
Db 4 KLRPNQVIVKLGRIIYLVGMWGSGKSTGPHLAKLLKYSFIDQDELIEK-VAKSVSQI 62

QY 141 FKVHSEAFPRDNESVLRDLSSMRRLVVATGGGAVIRPINRWYMKRGLSVWLDVPLDALA 200
Db 63 FREGENGFRDIETQVLKQIGORHSLVWATGGGLVTRSENWGLVHQGIVWLDPNRELLF 122

QY 201 RRIKVGTSAPRLDQPSGDPYAMAFSKLSMLAQOQGDYANADRVVSLEIETACKQGHDD 260
Db 123 ARLSKDKTVVRPLLD--NKDPKDV----LDSLIRKQRYLSYAEADLHISIE----- 166

QY 261 VSKLTPTDIAIESLHKIESFV 281
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0.75


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Db 115 VPEQLMQL-RADSTVRPLQTEPPD-----AALNALLNORRPLXAEADLTVINQETP 167
Qy 255 KQGHDDVSKLTPT 267
Db 168 LAVADGILQLLPS 180

RESULT 14
AROK SYNEL
ID AROK SYNEL STANDARD; PRT; 183 AA.
AC Q8DKH7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Shikimate kinase (EC 2.7.1.71) (SK).
GN Name=arok; OrderedLocusNames=tlr0882;
OS Synecococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
CC -I- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
CC -I- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC fifth step.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -I- SIMILARITY: Belongs to the shikimate kinase family.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC -----
CC EMBL; AP005371; BAC08434.1; -.
CC DR HSSP; P10880; 1SHK.
CC DR HAMAP; MF_00109; 1.
CC InterPro; IPR000623; Shik_kinase.
CC Pfam; PF01202; SKI; 1.
CC PRINTS; PR01100; SHIKIMTKINASE.
CC DR PROSITE; PS01128; SHIKIMATE_KINASE; 1.
CC Aromatic amino acid biosynthesis; ATP-binding; Complete proteome;
CC Kinase; Transferase.
CC NP_BIND 16 23 ATP (By similarity).
CC SEQUENCE 183 AA; 20778 MW; 98FAE2EE114CCA32 CRC64;

Query Match 20.4%; Score 311.5; DB 1; Length 183;
Best Local Similarity 43.3%; Pred. No. 4.9e-16;
Matches 71; Conservative 28; Mismatches 52; Indels 13; Gaps 5;

Qy 91 LNGRCIYLVGMGSKSTVGKIMSEVLGYSFSDSKLVEQAVGMPSPAQIFKVHSEAFPR 150
Db 7 LGGANIYLVGMWGAGKTTGRLLAQLRGLYSFVDTDAVI-TAFRQPIRIFAQEGEPAFR 65

Qy 151 DNESSVLRLDSMRRLVATGGAVIRPINWRYMKRGLSVLWLDVPLDALARRIAKVGTAS 210
Db 66 ELEQQVLAQVSSYHLVATGGGIVLNPWNWSYLLHHGIVVWLHVPLAVLCORLRQ--DRE 123

Qy 211 RPLL-DQPSGDPYAMAFSKLSMLAQQRGDAYANAD--VRVSLEE 251
Db 124 RPLLQEQPLEE-----RLGELLQARQHLXQAQDLRLTLED 160
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RESULT 15
Q7V904
ID Q7V904 PRELIMINARY; PRT; 192 AA.
AC Q7V904;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Shikimate kinase (EC 2.7.1.71).
GN Name=arok; OrderedLocusNames=PMT0163;
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Roca G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572095; CAE20338.1; -.
DR HSSP; P24167; 1KAG.
DR GO; GO:0005524; P.ATP binding; IEA.
DR GO; GO:0004765; P.shikimate kinase activity; IEA.
DR GO; GO:0008652; P.amino acid biosynthesis; IEA.
DR InterPro; IPR000623; Shik_kinase.
DR PROSITE; PS01128; SHIKIMATE_KINASE; 1.
CC Complete proteome.
CC SEQUENCE 192 AA; 20863 MW; B6F16CC52B622F76 CRC64;

Query Match 18.5%; Score 283; DB 2; Length 192;
Best Local Similarity 39.0%; Pred. No. 8e-14;
Matches 71; Conservative 27; Mismatches 64; Indels 20; Gaps 6;

Qy 91 LNGRCIYLVGMGSKSTVGKIMSEVLGYSFSDSKLVEQAVGMPSPAQIFKVHSEAFPR 150
Db 14 LGRNLYLVGMWASGKSTGRPLASQLSYGFVDTDAVIEQLAQGP-IPKIFSEEGAGPR 72

Qy 151 DNESSVLRLDSMRRLVATGGAVIRPINWRYMKRGLSVLWLDVPLDALARRIAKVGTAS 210
Db 73 TWESQVLAIGAQRHSLVATGGIYVKPENWGLVHGIVLWLNPGRELLRL-NADSGN 131

Qy 211 RPLLQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEETACKQGHDDVSKLTPTDIA 270
Db 132 RPLLQ--TEDPEA-AF---DCLFAERPLLYCEADL-----HVEVGAEBPDGIA 173

Qy 271 IE 272
Db 174 LK 175
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Search completed: August 25, 2005, 11:12:36
Job time : 67 secs

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OM protein - protein search, using sw model

Run on: August 25, 2005, 10:55:14 ; Search time 17 Seconds
(without alignments)
1726.242 Million cell updates/sec

Title: US-10-660-226-10
Perfect score: 1526
Sequence: 1 MEAGGVGLALQARAGFGSS.....ADSSASDAQESQIQRIOTL 305
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649.5	42.6	232	2 A84607	probable shikimate
2	642.5	42.1	300	1 S21584	shikimate kinase (
3	429	28.1	305	2 T09370	shikimate kinase h
4	338.5	22.2	181	2 A11961	shikimate kinase (
5	318.5	20.9	189	1 S74659	shikimate kinase (
6	249.5	16.3	168	2 A70487	shikimate kinase -
7	237.5	15.6	492	2 B72389	shikimate kinase/3
8	234.5	15.4	200	2 F87621	shikimate kinase (
9	224	14.7	173	2 AD0019	shikimate kinase (
10	223.5	14.6	174	2 C82053	shikimate kinase v
11	217	14.2	170	2 F81038	probable shikimate
12	217	14.2	173	2 AC1000	shikimate kinase (
13	216	14.2	240	1 A65134	shikimate kinase (
14	216	14.2	240	2 H91157	shikimate kinase I
15	216	14.2	240	2 F86003	shikimate kinase I
16	214	14.0	180	1 F64054	shikimate kinase (
17	210	13.8	173	2 H84992	shikimate kinase (
18	207	13.6	165	2 G97010	shikimate kinase (
19	203.5	13.3	172	2 H83015	shikimate kinase p
20	196	12.8	166	2 H98280	shikimate kinase (
21	191.5	12.5	162	1 S52581	shikimate kinase (
22	187	12.3	163	2 AH3002	shikimate kinase (
23	186.5	12.2	169	2 G86842	shikimate kinase (
24	186	12.2	162	2 AE3257	shikimate kinase (
25	179	11.7	171	1 AC0550	shikimate kinase I
26	178	11.7	173	1 S09613	shikimate kinase (
27	177.5	11.6	174	2 AP0390	shikimate kinase (
28	177	11.6	158	2 C95159	shikimate kinase (
29	176.5	11.6	174	2 A89934	hypothetical prote

30	176	11.5	158	2 C98025	shikimate kinase (
31	174.5	11.4	180	2 D82693	shikimate kinase x
32	173	11.3	157	2 AE1293	shikimate kinase h
33	173	11.3	157	2 AC1665	shikimate kinase h
34	171.5	11.2	199	2 E86973	probable shikimate
35	171	11.2	165	2 A81382	shikimate kinase (
36	162.5	10.6	238	2 A75478	shikimate kinase -
37	159	10.4	176	2 G70658	shikimate kinase -
38	150.5	9.9	275	2 D84769	hypothetical prote
39	150	9.8	174	1 KIECS	shikimate kinase (
40	150	9.8	174	2 F90683	shikimate kinase I
41	150	9.8	174	2 B85534	shikimate kinase I
42	147	9.6	186	1 I39782	shikimate kinase (
43	142.5	9.3	176	2 B72004	shikimate kinase C
44	141.5	9.3	162	2 E64539	shikimate acid kina
45	140.5	9.2	176	2 C86620	shikimate kinase I

ALIGNMENTS

RESULT 1

A84607

probable shikimate kinase precursor [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cross)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: A84607

R;Lin. X.; Kaul, H.; Moirfat, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

cus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420, MUID:20083487; PMID:10617197

A;Accession: A84607

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-292 <STO>

A;Cross-references: UNIPROT:Q9SJ05; GB:AE002093; NID:g4417286; PIDN:AAD20411.1; GSPDB:G

C;Genetics:

A;Gene: At2G21940

A;Map position: 2

C;Superfamily: shikimate kinase; shikimate kinase homology

Query Match 42.6%; Score 649.5; DB 2; Length 292;
Best Local Similarity 62.1%; Pred. No. 9.8e-45;
Matches 128; Conservative 36; Mismatches 41; Indels 1; Gaps 1;

QY 79 LKRRKSEEVLFYNGRCIYLVGMGSGKSTVGKINSVLGYGFFDSDKLVQAVGMPSVA 138

DB 88 ILKRKAEEYKPYLNGRSMYLVGMGSGKTTVGKLSKVLTGTFDFCDTLIEQAMNGTSA 147

QY 139 QIFKVHSEAFFRDNSSVLRLDLSMRLLVATGGGAVIRPINRWYMKRGISVWLDVPLDA 198

DB 148 EIFVHNGENFFKGTETDAUKSSRYQYVVVSTGGGAVIRPINRWYMKRGISVWLDVPLEA 207

QY 199 LARRIAKVAGTASRLPDQSPGYAMAFSKLSMAQQRGDYANADRVVSLEEIAKQGH 258

DB 208 LAHRIAACVCTDSRPLLDHSDGDAYSVAFKRLSAINDERGEAYTNANARVSLNIAAKRGY 267

QY 259 DVVSKLTPTPDIAIESLHKIESFVIEH 284

DB 268 KNVSDLTPTPEAIE-VSQVLSQLLHH 292

RESULT 2

S21584

shikimate kinase (EC 2.7.1.71) precursor - tomato

C;Species: Lycopersicon esculentum (tomato)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S21584

R;Schmid, J.; Schaller, A.; Leibinger, U.; Boll, W.; Amrhein, N.

submitted to the EMBL Data Library, December 1991

A;Description: In vitro synthesized tomato shikimate kinase precursor is enzymatically

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AD0019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-173 <KUR>

A;Cross-references: UNIPROT:Q8ZJF7; GB:AL590842; PIDN:CAC89014.1; PID:g15978256; GSPDB:G

A;Genetic:

A;Gene: aroK

C;Superfamily: shikimate kinase; shikimate kinase homology

C;Keywords: phosphotransferase

Query Match 14.7%; Score 224; DB 2; Length 173;

Best Local Similarity 35.5%; Pred. No. 8.1e-11;

Matches 59; Conservative 32; Mismatches 61; Indels 14; Gaps 6;

QY 94 RCYLVGMGSGKSTVGKTMSEVLGYSPFDSKLVQAVGMSPVAQIFKVHSEAFPRDNE 153

DB 5 RNIFLVGPMGAGKSTTGRLAQQLNMEFPDSQOEIRRTG-ADVGWVDFVEGEGFRDRE 63

QY 154 SSVLRDLSSMRRLVAVTGGAV-IRPINRWYMKRGLSVLMDVPLDALARRIAKVGTPASRP 212

DB 64 EKVINLTEKQGHVLATGGSVKSRTRNRLSARGVVVYLETIEKQLARTOR--DKKRP 121

QY 213 LL--DOPSGDPYAMAFSKLSMLAQQRDAYAN-ADVRVSLSEIACK 255

DB 122 LLQVDEPPRE-----VLENAKERNPLYEEIADVTIRTDDQSAK 160

RESULT 10

C82053

shikimate kinase VC2629 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: C82053

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: C82053

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-174 <HEI>

A;Cross-references: GB:AE004329; GB:AE003852; NID:g9657211; PIDN:AAF95770.1; GSPDB:GN001

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetic:

A;Gene: VC2629

A;Map position: 1

C;Superfamily: shikimate kinase; shikimate kinase homology

Query Match 14.6%; Score 223.5; DB 2; Length 174;

Best Local Similarity 34.1%; Pred. No. 8.9e-11;

Matches 60; Conservative 36; Mismatches 63; Indels 17; Gaps 7;

QY 94 RCYLVGMGSGKSTVGKTMSEVLGYSPFDSKLVQAVGMSPVAQIFKVHSEAFPRDNE 153

DB 5 RNIFLVGPMGAGKSTTGRLAQQLNMEFPDSQOEIRRTG-ADVGWVDFVEGEGFRDRE 63

QY 154 SSVLRDLSSMRRLVAVTGGAVIRPINW-RYMKRGLSVLMDVPLDALARRIAKVG-TASR 211

DB 64 EAVINDLTEQQGIVLATGGGSVSKSRNRLSARGIVVYLETIE---KQLARTNRDKK 120

QY 212 PLL--DOPSGDPYAMAFSKLSMLAQQRDAYAN-ADVRVSLSEIACKQGHDDVSKL 264

DB 121 PLLQTDPCR-----EVLEQAEDRNPLYEEIADITVRTDDQSAKVVAQIVKM 168

RESULT 11

F81038

probable shikimate kinase (EC 2.7.1.71) NMA0648 [imported] - Neisseria meningitidis (str

C;Species: Neisseria meningitidis

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: F81038; H81984

R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.;

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Accession: F81038

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-170 <TET>

A;Cross-references: UNIPROT:Q9JQV1; GB:AE002531; GB:AE002098; NID:g7227065; PIDN:AAF4214

A;Experimental source: serogroup B, strain MC58

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: A81775; MUID:20222556; PMID:10761919

A;Accession: H81984

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-170 <PAR>

A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83937.1; PID:g737937

A;Experimental source: serogroup A, strain Z2491

C;Genetic:

A;Gene: aroK; NMB1813; NMA0648

C;Superfamily: shikimate kinase; shikimate kinase homology

C;Keywords: phosphotransferase

Query Match 14.2%; Score 217; DB 2; Length 170;

Best Local Similarity 37.1%; Pred. No. 2.9e-10;

Matches 62; Conservative 30; Mismatches 61; Indels 14; Gaps 8;

QY 92 NGRCYLVGMGSGKSTVGKTMSEVLGYSPFDSKLVQAVGMSPVAQIFKVHSEAFPRD 151

DB 5 NKKLI-LIGLMGAGKTTILGROAQRDLRYFYDSDEHIAAAGVP-IPTIFEMEGQGFRS 62

QY 152 NESSVLRDLSSMRRLVAVTGGAVIRPINRWY-MKRLSVLMDVPLDALARRIAKVGTPAS 210

DB 63 RETAILKKLVILPHVLSTGGAVLKEENRALIRKSTGVVYLHAPETLLERTR--CDNS 120

QY 211 RPLDQPSGDPYAMAFSKLSMLAQQRDAY-ANADVRSLSLEIACKQ 256

DB 121 RPLQ--VADPLA----KLRELYAARDPVYRQTADFTV--ESANCRE 159

RESULT 12

AC1000

shikimate kinase (EC 2.7.1.71) - Salmonella enterica subsp. enterica serovar Typhi (stra

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AC1000

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

. S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AC1000

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-173 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD08127.1; PID:g16505106; GSPDB:GN00176

C;Genetic:

A;Gene: aroK

C;Superfamily: shikimate kinase; shikimate kinase homology

C;Keywords: phosphotransferase

Query Match 14.2%; Score 217; DB 2; Length 173;

Best Local Similarity 32.4%; Pred. No. 3e-10;

